

	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360		
HOARCCRPGVWSPDAARGLSVCRCCRLHPASAMDLFGDLPPEPSPPPAPAGKEAGKGLPLFFDLPASTT																																						
10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360			
SSGGPILFFDLPASSGGSLATSIOWKTEGKGAKRKTSSEKKNKSGSELYEKKVCASSVFGKGYG																																						
SSGGPILFFDLPASSGGSLATSIOWKTEGKGAKRKTSSEKKNKSGSELYEKKVCASSVFGKGYG																																						
80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430			
APRKKEPMDAVALINDITECPPESSLTRVSYAYVADGGIGRASKPAONLHONIRKPEKGPISV																																						
APRKKEPMDAVALINDITECPPESSLTRVSYAYVADGGIGRASKPAONLHONIRKPEKGPISV																																						
150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500			
AKRKKEPMDAVALINDITECPPESSLTRVSYAYVADGGIGRASKPAONLHONIRKPEKGPISV																																						
AKRKKEPMDAVALINDITECPPESSLTRVSYAYVADGGIGRASKPAONLHONIRKPEKGPISV																																						
150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500			
EXTVRCILDTFKTDEEPKQASSQKPAKMOGSTATCVLADNLTLYANTGDSRALTLCRYNEESKPAALS																																						
EXTVRCILDTFKTDEEPKQASSQKPAKMOGSTATCVLADNLTLYANTGDSRALTLCRYNEESKPAALS																																						
220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570			
LSSEINPFOYERERRRLOKAGGVNRGGRVLGYLVEVSRISIGDQYKRCGVTSVPDIRCOLTNPDIRPLIACDQ																																						
LSSEINPFOYERERRRLOKAGGVNRGGRVLGYLVEVSRISIGDQYKRCGVTSVPDIRCOLTNPDIRPLIACDQ																																						
190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	3																					

350 340 350 360 370 380 390 X
LEKVTPEEAVNFILISCEDEKIQITREGKSAADARYEACNRLANKAVORGADNVTVMVVRIGH
LFKVTPEEAVNFILISCEDEKIQITREGKSAADARYEACNRLANKAVORGADNVTVMVVRIGHXGVARGO
370 380 390 400 410 420 X 430
EHAWYXLRFFILCCTCTVCTVGLPMLXIVSLFFPPKKK
440 450 460 470

2. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A

GENERAL INFORMATION:

APPLICANT: Lorens, James

APPLICANT: Xu, Weiduan

APPLICANT: Atchison, Robert

APPLICANT: Bogenberger, Jakob

TITLE OF INVENTION: Modulators of Angiogenesis

FILE REFERENCE: 021044-000210us

CURRENT APPLICATION NUMBER: US/09/935,124A

CURRENT FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 1422

TYPE: DNA

ORGANISM: Homo sapiens

Initial Score = 14 Optimized Score = 24 Significance = -0.37
Residue Identity = 24 Matches = 31 Mismatches = 69
Gaps = 26 Conservative Substitutions = 0
Translation Frame = 6

FFLGKRETFIYNHSGPTGKHTNVHTHKMNLISQYHACSWPRATPOCPITRTITVTLSABPRCTALASTL
10 20 30 40 50 60 70
LOAASXBSAADPSPRNVITFSSSRDOKMFTASSGVKTLSQSPQANKMNLISGVSMQRLMSGTEVTYPORLYC
80 90 100 110 120 130 140
PSPMERDTSSTREKTPSLTPPAPFCILIRSSYXVGLCSLLRLKAACFXLSLXRNKIALSPRLAIXRMLST
150 160 170 180 190 200 210
ARTHAVDPSPQAGWLEACLRNSSVCLKVKRHLFTVFTLITSPLGNFLIKFKCKCANFEARIPPCP
220 230 240 250 260 270 280

SKTAKYETRVMBDDGLHSSVMSFNTWASCISSLPFRSATXPPRPKITEBALQTFSTSSSLPFPSSSEV
290 300 310 320 330 340 350 360
DLFGDLP-----EPERSPPRAG-KEAQKPLFDLPPASSTDSGGGGLLFDLPPASGDSG
370 380 390 400 410 420
FLFAFPFVFTTWDIVAREPE-SPLLAGGSSKSKGPPDPESVLLAGRSSKSKGP--FXASFPRA----AG
70 80 90 100 110 X 120 130
SLATISQGVKTEGKAGKRTSEEEKNGSEELVEKKVCRAASVIFGLKGYVABERKGEREMODAVIINDIT
140 150 160 170 180 190 200
RGERGS-----GRSPKSMALAGHRROQOTLSPRAAAGLHTPGGRORAM
430 440 450 460 470 X

140 150 160 170 180 190 200
EBCRPSSILITVSVFAVVDHGGRASKAFAONLHQNLIRKFKGDIVSVEKTVKRCCLDTDFKHTDEEFLK
210 220 230 240 250 260 270
QASSOKPAWKDGSTATCVLADNLTLYIANLGDSSRALICRYNEESQHAALSLSKHNPTQYEBERWRIQKAGG

280 290 300 310 320 330 340
NVRDRVLGVLEVSISDGOYKRGCVTSVPDIRRCQUTPNDRFILLACDGLFKVFTPEEAVNFILISCEDE
350 360 370 380 390
KIQTREGKSAADARYEACNRLANKAVORGADNVTVMVVRIGH

3. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A

GENERAL INFORMATION:

APPLICANT: Lorens, James

APPLICANT: Xu, Weiduan

APPLICANT: Atchison, Robert

APPLICANT: Bogenberger, Jakob

TITLE OF INVENTION: Modulators of Angiogenesis

FILE REFERENCE: 021044-000210us

CURRENT APPLICATION NUMBER: US/09/935,124A

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: 60/284,760

PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 1422

TYPE: DNA

ORGANISM: Homo sapiens

Initial Score = 8 Optimized Score = 72 Significance = -0.41
Residue Identity = 21 Matches = 100 Mismatches = 254
Gaps = 101 Conservative Substitutions = 0
Translation Frame = 5

FFFRKKKNLYLQPMESHSTONTQCAHTONEBPKSIPCVLLAARHPSVPYRHHNSDVNGRAPLHRVGGP
10 20 X 30 40 50 60 70
MDLFGDLPPEERS-----PPRACKERAKG--PL-LFDLPL
10 20 30 40 50 60 70

PASSTDSGGGGLFDLPPASGDSGLATISOMVTEGKAKRKISEERKNG-SEELVEKKVCRAASV
40 50 60 70 80 90 100
VAGCFVAVGGGLPFGPGL-----DLFLET-GODEVHGFVG--KDLBERTGOQNEPVGOLAAADV-
80 90 100 110 120 130

110 120 130 140 150 160 170
FGLKGYVABERKGEREMODAVIINDITBECRPPSSLITRVSVFAVVDHGGRASKAFAONLHQNLIRKFP
140 150 160 170 180 190 200
-GHRGDTA-ALVLPVNGAXHLXHAQNTPIPDVSSSLDYPHPLFTLSWIMLFAEXXGCMFLTL--LIITTO
140 150 160 170 180 190 200

180 190 200 210 220 230
KGDVSS--VEKTV-----KR-----CLL--DTFKHTDEEFLKQASSQAPAMKDGSTATCVLADNLT
210 220 230 240 250 260
DCPTISEGNIKNVVYSONTGSGLPIPGRLAGSLFKELFTISM--ESVOK-ASLHGFLYT-----DY
210 220 230 240 250 260

140 150 160 170 180 190 200
ISFRFSDXVLMQILCSFKXGSSNSMSIKSKIXNP--SNEGKMGFTLLGDVQDDVGILHLPLTLPLSHIA
270 280 290 300 310 320 330
IANTLGS---RAILCRYNEESQKALSLSKHNPTQYEBERWRIQKAGNVRD--GRVLGVLEVSISGD
240 250 260 270 280 290 300

300 310 320 330 340 350
GOYKRCGVTSVPDIRRCQUTPNDR-----ILLACDGLFVFTPEEAVNFILISCEDEKIQITREG-----
270 280 290 300 310 320 330
LQTK-----DHR--GFTNPLFKRLFTAILLFLGFSLCSFPFSLYHNGYXGKRTXIATAGWEIHK
340 350 360 370 380 390

-----XSAADAR--YEAACNRLANKAVORGADNVTVMVVRIGH
360 370 380 390 X
-----XSAADAR--YEAACNRLANKAVORGADNVTVMVVRIGH

ORSPKXVSTACRREVIKEGCSFLSPFGSRARRALGLRQVPEEYHGCGWVEAATDTTOPASSGRAPHPGR
400 410 420 430 440 450 460
AAAAGL
470

4. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A
GENERAL INFORMATION:

APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 1422
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score = 6 Optimized Score = 37 Significance = -0.42
Residue Identity = 17% Matches = 47 Mismatches = 191
Gaps = 38 Conservative Substitutions = 0
Translation Frame = 2

MDLFDLPEPERSPPRPAAGKAOKGPLLFDLPPASSTDSGSGGPLLFDLPPASGDSGLATSIQWVKT
80 90 100 110 120 130 140 150
EGKAKRTSEBEKNGSEBELVEKVCASVIFGLKGYAERKGEREMODAHVILNDITECRPSSLITR
VSFAVFDHGIGIRASKFAQNLHONLIRKFKPGDVISVEKTVKCLDITFKHTDEEFLKQASSQKPAWKDG
150 160 170 180 190 200 210
PPARVERP-RCSRAECLSLPPPSLRHGPRLRGPLRGPAARALAPGCRERSERTPALXXPPSGQGYXLRING
20 30 40 50 60 70
STA-----TCUAVNITLIYINLIGDSRALICRYNESQKHALSISEHNPTOYERMRIOKAGSNVDDGV
220 230 240 250 260 270 280
TFPFXSPTRXOMRFRFSCHINIPDGDKRER-----SUEKILRGEE-MOXRAKGESLSL
80 90 100 110 120 130
LGVLEVSRSITGGQYKRCGVTSPDIRRCQLTNDFFILLACDGLFKVTPBEAVNFI--SCLF-----DE
140 150 160 170 180 190 200
FGGLSEGLCGAEGEGDAGCPRPERRHRCVXAPIVPHYSGITFCCEFXMTWNSLKTICTTEBASLNO
210 220 230 240 250 260 270
KLSXRCCNOCRENREEMPFHQAYYXXRVXTSFQPEACLERWVCHVCSQCRQSHLYCOPRXSGNLSIX
280 290 300 310 320 330 340 350
XGESKTSCLKPOQRAKSNVXRADDETEGWRKSGWACFGARAGVTLLHMGRAVOALRCHLCARHQTLPADPQ
360 370 380 390 X
KIOTREKSAADARYE-----AACRLNKAQVGSADNVTV-MVVRIGH
KLSXRCCNOCRENREEMPFHQAYYXXRVXTSFQPEACLERWVCHVCSQCRQSHLYCOPRXSGNLSIX
210 220 230 240 250 260 270
XQVHFWGLXWALQGLYPRRSREHLVLVSRGXKDPDPRGEVRERRPLRESLQAOAGCGAAGLGRQRHCDGGA
360 370 380 390 400 410 420

DRLRGARPGAMVITXKVFVCHIVCYVSGCTPMMVNNKGFSEFSKXK
430 440 450 460 470

5. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A
GENERAL INFORMATION:

APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 1422
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score = 6 Optimized Score = 28 Significance = -0.42
Residue Identity = 18% Matches = 39 Mismatches = 131
Gaps = 42 Conservative Substitutions = 0
Translation Frame = 4

MDLFDLPEPERSPPRPAAGKAOKGPLLFDLPPASSTDSGSGGPLLFDLPPASGDSGLATSIQWVKT
80 90 100 110 120 130 140 150
EGKAKRTSEBEKNGSEBELVEKVCASVIFGLKGYAERKGEREMODAHVILNDITECRPSSLITR
VSFAVFDHGIGIRASKFAQNLHONLIRKFKPGDVISVEKTVKCLDITFKHTDEEFLKQASSQKPAWKDG
150 160 170 180 190 200 X 210
FTTNGV---DQETKMTWCTHKKCFXVNTWRAGRAPPLSLASAPPSQXRCRPSAPAPPCWACCRL--
20 30 40 50 60 70
290 300 310 320 330 340 350
EVSISIDGQYKRCGVTSPDIRRCQLTNDFFILLACDGLFKVTPBEAVNFI--SCLF-----DE
---RS---GRRLR---TSLP---GSGSFHPRDKTXSSRLILGKRPRAHHRPTKXTCHWSAGSYCKRAQK
80 90 100 110 120 130
GKSNADRYEACNRLLA-----NKAVORGSA---DNVTVMVVRIGH
140 150 160 170 180 190 200 210
HRSACTARPMQSVYTLARAKNAHPKRFLOPSVSSALHTLTDALCXGLRHVFDSPHYNDTRLPDYLRGW
220 230 240 250 260 270 280
YKECCLQPEHTWQTHLSRQASGWLXGTLHQAACPKPKGISRSLSLXLHLKLEIFXLSFDANSVOQILR
290 300 310 320 330 340 350
LEFLHVAQKOONKRPKXQKTMGAVTPRXCRSGKRGHPSPHSAQSPSDORSFRLYKLSFQALHCH
360 370 380 390 400 410 420
AASAPADAGPRRGPMWRLLGGGSSDRHSARFORPGSTPRAGSSSPG
430 440 450 460 470

LFEEUXXX
470

6. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A
GENERAL INFORMATION:

APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Alchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 02104-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1422
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score = 6 Optimized Score = 49 Significance = -0.42
Residue Identity = 188 Matches = 69 Mismatches = 213
Gaps = 95 Conservative Substitutions = 0
Translation Frame = 1

MDLFGDLPPEPSPRPAAGKEAQKGPLLPDDLPPASSTSGSGGPLLPASSGDSGLATISIQWVT
|
GT
X

80 90 100 110 120 130
EGKGAKRTSEEEKSGSEELVEKTYCKA-----SSVIFGLKGYVAERKGEREMQDAHYIINDITE
| | | | |
RPAAR-----PGGARPLAGXVVAASSTOPPWTSGTCSRSPARARLPQKLRKD-----
10 20 30 40 50

140 150 160 170 180 190
ECRPPSSLITRVSFAVNDGHHG-----IRASKFAA---ONT--HONLRKFPKGDVISEKTVK----CLL
| | | | |
---PCSLMT-SLRPAVLTDQDGLCFIMISHPLVALQVLLPHQYPMXRLKGEQREKPPRRKRMAYKSL
60 70 80 90 100 110 120

200 210 220 230 240
DTFKHTDEEFLK--QASSOKPA--WKDG-----STATCVLAVDNITLYIANLGDRAILCRYNESQ
| | | | |
WKRK-----FVAPLXSLVXRAMWLSGRVGRRCMPSTSTTSPPRSV-----GPRPSL-----LG
130 140 150 160 170

250 260 270 280 290 300
KHAALSL--SKEHNPTQYERMRIOKAGN-----VRDGRVIGVLEVSRSITGDQYKRCGVTSVP
| | | | |
FILFLFLMDMEFEFQNLHRCITXSENFLKEMXSVYRKPRDAFWTLSSILMKSSINKLPAKSLPGKWG
180 190 200 210 220 230 240 250

310 320 330 340 350 360 370
DIRRQQLFNDRFL--LACDGLFKYFTPEBAVNFILSLGLEDEKIQTRREGKSAADARYEACNRLANKAVQR
| | | | |
PLPRVFWLXTFFLPTSEIVGQSCVIMRRVKNMQPKASAKSIQLSMKSGXGYRLEETSGMGVFWACXR
260 270 280 290 300 310 320

380 390 X
GSADNVTVWVVRIGH
|
CHAPLGTSTSAVAAPLCPTSDAASXPFMTGSFCWPVMGSSRLPQKKEPTSSCPVSRMKRGRPGKSGPQPT
330 340 350 360 370 380 390

PATQDPATGWPTRRCGAPRTTSLXWMCXGTEGWRBAASHTGIDLKSGFCVCAHCVFCVLLMDSHGCKKRF
400 410 420 430 440 450 460

US-09-935-12A-1 (1-1422) x G66315 (1-341)

Qy	333	AAAGAAAAA	CTCCGAGAAAGAGAA	GAATGGCA	GTGAAAGACTTGTC	-----	380
Db	24	Lyvala	Lyvala	Lyvala	Lyvala	Lyvala	43
Qy	381	---GAA	AAGAAGT	TTGTA	AAGCTCTTGCGTATC	-----	422
Db	44	ArgGlu	ArgGlu	ArgGlu	ArgGlu	ArgGlu	63
Qy	423	AAGGCTAT	TGTCGTGAGCGGAA	GGGTGAGAGAGAG	AGATGCGAGGATGCCACGCTCATC		482
Db	64	Glu	Ala	Ala	Ala	Ala	83
Qy	483	CTGAAC	CAATCATCCGAGAG	TGTAGGCCCCCATCGCTCATTA	CTCGGTTTCATAT		542
Db	84	Leu	Pro	Ala	Ser	Leu	99
Qy	543	TTTGCTG	TTTTGATGACAT	TGAGAGAA	TTTCAGGCTCCAAAATTTCCTCAGAAATTTG		602
Db	100	Phe	Ala	Ile	Arg	Glu	119
Qy	603	CATCAAA	CTTAATCAGAAAA	TTTCTCTAAAGAGATGTA	TACGTATGAGAAAAACCGTG		662
Db	120	His	Leu	Met	Val	Leu	138
Qy	663	AAGA	ATGCTTTTGGACACT	TTTCAGACATATCATG	ATGAAGAGTTCTCTTAACAGCTTCC		722
Db	139	Leu	Val	Ala	Ile	Leu	158
Qy	723	AGCC	AGAACTGCTCGGAA	AGATGGTCCACATG	CCACGCTGTTTGGCTGTACACAC		782
Db	159	Ser	-----	Gly	Ile	Pro	176
Qy	783	ATTCTT	TATTTTGGCAACT	CGGAGATGATCGGGCA	TATCTGTGCTGCT	-----	830
Db	177	Leu	Val	Ala	Ala	Ala	196
Qy	831	-----	TATTA	TAGAGAGATCA	AAAAACATGACACCTTAA	GCTCAGCAAA	875
Db	197	Arg	Glu	Leu	Glu	Ala	216
Qy	876	GAGCA	TAACTCAACT	CAGATGAAAGACGGATG	AGATACAGAGGCTGGAGAAAGCTC		935
Db	217	Glu	His	Val	Ala	Ile	236
Qy	936	---AGG	ATGGCGCGT	TTTTGGCGCTGCTA	AGAGGTGACCGCTCAATGGGGACGGGACG		992
Db	237	Ser	Arg	Ala	Glu	Ala	256
Qy	993	TACA	AGCGCTCGGCTG	TACCTCTGTGCCAGATCA	GAGCGCTGCACGCTGACCCCAAT		1052
Db	257	Phe	Leu	Val	Ala	Ala	276
Qy	1053	GACA	GGTTCAATTTGTTGG	CTGTGATGGGCTCTTCA	AGGCTTTTACCCCAAGAAAGCC		1112
Db	277	Glu	Ala	Ala	Ala	Ala	296
Qy	1113	GTGA	ACTTCACTCTGCTCTG	TCTGAGAGATGAAA	AATGATCAAGCCCGGGAAGGAAGTCC		1172
Db	297	Val	Glu	Ala	Ala	Ala	307
Qy	1173	GCAG	CGGACGCCCTGAC	AGAGACGCTTGCA	ACAGGCTGGCAACAGCGGCTG---CAG		1222
Db	308	-----	Leu	His	Val	Ala	324
Qy	1230	CGGG	CTCGGCGGCAAC	AGTCACTGTGATG	TGATGATGATG		1265
Db	325	Arg	Arg	Cys	Leu	Ala	336

RESULT 2
118388,
probable protein phosphatase - Caenorhabditis elegans

```
C:\Species: Caenorhabditis elegans  
C:\Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999  
C:\Accession: T18588; T21693  
submitted to the EMBL Data Library, December 1998  
R.Mortimore, B.  
A.Reference number: Z18993  
A.Accession: T18588  
A.Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: DNA  
A.Residues: 1-242 <Wt>  
A.Cross-references: EMBL:AL031264; PIDN:CNA20326.1; GSPDB:GN00020; CESP:F33A8.6  
A.Experimental source: clone VF45E10L  
R.Mathews, L.  
submitted to the EMBL Data Library, November 1996  
A.Reference number: Z19459  
A.Accession: T21693  
A.Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: DNA  
A.Residues: 1-242 <Wt>  
A.Cross-references: EMBL:Z81525; PIDN:CA804260.1; GSPDB:GN00020; CESP:F33A8.6  
A.Experimental source: clone F33A8  
C.Genetics:  
A.Gene: CESP:F33A8.6  
A.Map position: 2  
A.Introns: 28/1; 65/2; 101/1; 133/2; 202/2
```

```
Alignment Scores:  
Pred. No.:      3,61e-29      Length:      242  
Score:          474.00        Matches:     98  
Percent Similarity: 62.30%    Conservative: 50  
Best Local Similarity: 40.16% Mismatches:     84  
Query Match:    18.52%       Indels:      12  
DB:             2            Gaps:         5
```

```
US-09-935-124A-1 (1-1422) x T18588 (1-242)  
QY      345   TCCGAGGAAGAAGAAATGGCAGTGAACGCTTG-----GAAAAGAACTT   392  
           |||:::| | | | | | | | | | | | | | | | | | | | |  
Db       3   SerApSerArgLySargSerSerSerApSerPheLeuIleApaSenSerApGlySerLySlys  22  
           |||:::| | | | | | | | | | | | | | | | | | | | |  
QY      393   TGTAAGCGCTTCGTGANTCTTTGTGTCTGAAGGGCTATGTGGCTGACGGAGGGGTGAG  452  
           ||| ||| | | | | | | | | | | | | | | | | | | | | |  
Db       23   ProLySgluSerArgAsnleuTyCySThrleuAlaIaTyRgLyCySArgLySglu  42  
           ||| ||| | | | | | | | | | | | | | | | | | | | | |  
QY      453   AGGGAGGATGCAGATGCCACCAGCTCATCTCTGAAC-----GACATCACCGAGAGTGT  506  
           ||| ::|||::| | | | | | | | | | | | | | | | | | | | |  
Db       43   ArgAlaapMetGlnApRThrHieIleMetleuProLySPhaeApLeuGlYThcglu---  61  
           ||| ::|||::| | | | | | | | | | | | | | | | | | | | |  
QY      507   AGGCCCCCATCGTCCCTCATTACTGGGGTTTCATATTGTCGTGTTTGGTAGGACATGGA  566  
           ||| ::|||::| | | | | | | | | | | | | | | | | | | | |  
Db       62   -----LysSerPheLeuSerArgLaSerPhePheAlaIlePheApGlyHisAla  78  
           ||| ::|||::| | | | | | | | | | | | | | | | | | | | |  
QY      567   GGAATTGCAGGCTCAAATTTGCTGCACAGAATTTGCATCAAACTTAATCAGAAAAATT  626  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
Db       79   GlyProAlaGlaAlaIaGluHieCySglInserGlnMetGlyLyTrmValLySgluLySleu  98  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
QY      627   CCTAAA----GGAGATGTATCAGTGTAGAGAAAACCGTGAAGAGATGCTTTTGACACT  683  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
Db       99   AlaLySpheSerApPheProThreuthrLySserLeuLySglInThrPheTherGluSer  118  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
QY      684   TTCAGACATCTGATGAAGAAGTTCCTTAAACAAGCTTCACGCCAGACGAGCTGCTGAAA  743  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
Db      119   TyrLySAlaValaIaSpApGlyPheLeuAlaIleAlaLySglInAenLyProIleTryps  138  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
QY      744   GATGGGTCCACTGCGACAGCGTGTCTTGCGCTGTAGAACATTTCTTATATGCGCAACTC  803  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
Db      139   ApRgLyThrThrAlaIaThrThrMetIleIleLeuEnaAnVaIlIetyValaIaasnIle  158  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
QY      804   GGAGATAGTCGGCGGCACTGTGTCGTTATATAGAGAGTCAAAACATGACGACCTTA  863  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
Db      159   GlyApSerArgAlaValaIaAlaRgLySlySgluApGly---SerPheAlaProVal  177  
           ||| ||| ||| | | | | | | | | | | | | | | | | | | | | |  
QY      864   AGCCTCAGAAAGACATATCCAATCAGATGAAGAAGCGATGAGGATACAGAAGCT  923
```


US-09-935-124a-1 (1-1422) x 562462 (1-414)

```
OY 342 ACCTCCGAGAAAGAAAGTGGCACTGAAAGCTTGGAAGAAAGTTGTAAAGCC 401
    |||:::|||||
DB 10 ThrGluLysHisSerValIleGlySerIleGluPhe----- 21
OY 402 TCTTCGGTCACTTTGGTGTGAAGGGCTATGTGCTGACGGGAAGGTGAGAGGAG 461
    |||:::|||||
DB 22 -----ValLeuTyrGlyLeu-----SerSerMetGlnGlyTyrPheGlySer 35
OY 462 ATGCAAGAGATCCAGATCCTCGAAGACATACACCGAAGCGTATGAGCCCATGCTCC 521
    |||:::|||||
DB 36 MetGluAspAlaHisSerAlaIle-----LeuSerMetGluLys-----SerAla 50
OY 522 CTCATTAATCTCGGTTTCATATTTGCTGTTTGTATGATGACATGAGAAATTCAGCCTCA 581
    |||:::|||||
DB 51 ValLysAspProValAspPhePheIleValTyrAspGlyHisGlyLysAspValAla 70
OY 582 AAAATTTGTCACAGAAATTTGCATCAAACTTAATCAAGAAA-----TTTCCTAAAGCA 635
    |||:::|||||
DB 71 LysTyrCysGlySerAsnLeuProGlnIleLeuGluLysAsnProAspPheGlnLysGly 90
OY 636 GATGTAATCAAGTCTAGAGAAAAC-----CTGAAGAGATGCTTTTGTGACACT 683
    |||:::|||||
DB 91 AspPheValAsnAlaLeuLysSerSerPheLeuAsnAlaAspLysAlaIleLeuAsp--- 109
OY 684 TTCAAGCATCTGATGATGAAGATCTCTTAACAAGCTTCCAGCCAGAAAGCTGCTGAAA 743
    |||:::|||||
DB 110 -----AspAspGlnPheHisThrAspProSer----- 118
OY 744 GATGGGTCACTGCCACGTGTGTTGCTGCTGTAAGACAACTTTATATGCAACCTTC 803
    |||:::|||||
DB 119 ---GlyCysThrAlaThrValValLeuArgValGlyAsnLysLeuTyrCysAlaAsnAla 137
OY 804 GGAAGATGTCGGGCAATCTTGCTCTCTTAATGAGAGAAGTCAAAAGATGAGCCTTA 863
    |||:::|||||
DB 138 GlyAspSerArgThrValLeu-----GlySerLysGlyIleAlaLys 151
OY 864 AACCTCAGCAAGAGCATATCCAACTCAGTATGAGAGCGATGAGATACAGAGCT 923
    |||:::|||||
DB 152 ProLeuSerAlaAspHisLysProSerAsnGluAlaGlnLysAlaArgLysAlaAla 171
OY 924 GGAAGAAAGTGAAGGATGGGCGGTGTTGGGCGTCTAGAGCTCACGCTTCATGGG 983
    |||:::|||||
DB 172 GlyGlyPheValAspPheGlyArgValIleGlyAsnLeuAlaLeuSerArgAlaIleGly 191
OY 984 GACGGGCACTACAGCGCTCGCT-----CTCACCTCTGCGCC 1022
    |||:::|||||
DB 192 AspPheGluPheLysAsnSerAsnLeuGluProGluLysGlnIleValThrAlaLeuPro 211
OY 1023 GACATCAGACGCTGCCAGCTGACCCCAATGACAGGTTCATTTGTTGGCTGTGATGG 1082
    |||:::|||||
DB 212 AspValValAlaHisGlnIleThrAspAspAspGluPheValAlaLeuAlaCysAspGly 231
OY 1083 CTCTTCAGAGCTTTTACCCCAAGAAAGCGTGAACTTCTGTCTGTCTGAGAT 1142
    |||:::|||||
DB 232 IleTyrAspCysLysThrSerGlnGlnValIleGluPheVal----- 245
OY 1143 GAAAAGATCAGAACCCGGGAAGGAAGTCCGACGCCGACCCGCTACAGAGAGCC--- 1199
    |||:::|||||
DB 246 -----ArgArgGlyIleValAlaGlyThrSerLeuGluLysIleAlaGlu 260
OY 1200 -----TGCAACAGCGTGGCCACAAAGCGCGTGCACGGGGG---TCGGCCGCAAC 1247
    |||:::|||||
DB 261 AsnLeuMetAspPheCysIleAlaSerAspThrGluThrIleGluLysCysAspAsn 280
OY 1248 GTCACTGTGATGGTGTGGATGGGCACTGAGGGGTGGCGCGCCGACAGACAGCA 1307
    |||:::|||||
DB 281 MetThrValCysIleValAlaLeu-----LeuGlnGluLysAspLysSerAla 296
OY 1308 TGGTAT 1313
    |||:::|||||
DB 297 TrrTyr 298
```

RESULT 5

T08606

protein phosphatase 2C-like protein Spalten - slime mold (Dictyostelium discoideum)

C/Species: Dictyostelium discoideum

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C/Accession: T08606

R/Audry, L.; Firtel, R.A.

submitted to the EMBL Data Library, August 1997

A/Reference number: Z16454

A/Accession: T08606

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-975 <AUB>

A/Cross-references: EMBL:AF019985; NID:g2425120; PID:g2425121

A/Experimental source: strain AX3

C/Genetics:

A/Gene: spna

Alignment Scores:

Pred. No.:	7,47e-21	Length:	975
Score:	370.00	Matches:	126
Percent Similarity:	41.03%	Conservative:	57
Best Local Similarity:	28.25%	Mismatches:	164
Query Match:	14.45%	Indels:	99
DB:	2	Gaps:	19

US-09-935-124a-1 (1-1422) x T08606 (1-975)

```
OY 5 CCAGGCCGCTGCTGCCGCCGCCGCGGGGTGTGAGCCCGCGCTGCTCGCGGCTGAG 64
    |||:::|||||
DB 539 ProLysProValLysProProLysGluProLysProProLysGlu----- 613
OY 65 TGTCTGTGCTGCTGCGCCCTCCACCAAGCCTCGCCATGACCTCTTGGGAGACTGCC 124
    |||:::|||||
DB 614 -----ProLysProProLys-Glu-----Pr 620
OY 125 GGAGCCGAGCGCTGCGCGCGCGCGCTGCGCGGAAGACTCAAGAACCCCTGCT 184
    |||:::|||||
DB 620 OlyAspProLysGluProLysProLys-----LysGluProLysGluLysProValLys 638
OY 185 CTTGATGATCACTCCTCGCGCCAGAGATGATGATCAAGATCAGGGGAACTTGTCTTT 244
    |||:::|||||
DB 638 B---GluSerLysProProLysGlu----- 645
OY 245 TGAATATCTCCACCGCGCTAGACAGTGGGATTCAGTCTCTTGCACATCAATCCCA 304
    |||:::|||||
DB 646 -----ProLysProLysGluProLysGluSerLysGluProLysGluProLys 662
OY 305 GATGCTAAAGACTGAAGGAAAGAGCAAGAAAGAAACCTCC----- 347
    |||:::|||||
DB 662 GdluProLysProThrLysProProLysGluLysLysThrSerLysValAspGlyAlaAl 682
OY 348 -GAGAGAAAGAAATGCACTGAAGACTT-----GTGAAAAGAAAGTTTG 394
    |||:::|||||
DB 682 agLysLysLysAsnGlyAlaAspSerCysGlyAsnGlyValGlySerLysIleLys 702
OY 395 TAAAGCTCTTCGGTGATCTTGTCTGTGAAGGCTATGTGCTGAGCGGAAGGTGAGAG 454
    |||:::|||||
DB 702 sLeuGluSerLys-----PheGly-----SerLeuGlnGlyArgArg 714
OY 455 GGAGAGATGAGATGCGCCACGTATCTGAAACAGATCACCCGAGAGTGTAGG----- 509
    |||:::|||||
DB 714 GlyAsnMetGluAspThrHisValIleLeuLysAsnLeuMetGlyAlaValThrTyrAs 734
OY 510 -----CCCCATGCTCCCTCATTAATCTCGGGATTTCATATTTGCTGTTTGTGATGACATGG 565
    |||:::|||||
DB 734 nGlyProProLysAspIle-----ProLysSerLysThrAlaValTyrAspGlyHisGly 752
OY 566 AGGAATTCGAGCTCAAAATTTGCTGCACAGAAATTCATCAAACTTAATC-----AG 619
    |||:::|||||
DB 752 yGlyThrGluThrSerThrLeuLeuGluProThrValHisAsnCysLeuValAsnSerG 772
```



```
RESULT 7
T52337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C:Accession: T52337
R:Miyaoka, S.; Bohner, H.J.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999
A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcripts
A:Reference number: Z26045; MUID:99200489; PMID:10102366
A:Accession: T52337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MI>
A:Cross-references: EMBL:AF075580; PIDN:AAC36698.1
C:Genetics:
A:Gene: PPC
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
C:Keywords: phosphoric monoester hydrolase

Alignment Scores:
Pred. No.: 1,456-20 Length: 359
Score: 365.00 Matches: 92
Percent Similarity: 52.25% Conservative: 59
Best Local Similarity: 31.83% Mismatches: 94
Query Match: 14.26% Indels: 44
DB: 2 Gaps: 10

US-09-935-124a-1 (1-1422) x T52337 (1-359)
QY 447 GGTGAGAGGAGAGATGCAAGATGCCACGTCATCTGAACGACATCCAGAGG--- 503
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 58 GlyProArgLysTyrMetGluAspGluHisLeuArgIleAspAspLeuSerValGlnLeu 77
QY 504 -----TGTAAGCCCATGTCGTCCTCATTACTCGGGTTTCATATTTGCT 548
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 78 GlySerLeuPheArgCysProLysProSer-----AlaPheTyrGly 91
QY 549 GTTTTGGATGACATGAGAGAAATTCGAGCTCAAAATTGCTGCACAGATTGATCA 608
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 92 ValPheAspGlyHisGlyLysSerGluAlaAlaIleTyrValArgGluAsnValMetArg 111
QY 609 AACTTAATACAG-----AAATTCTTAAGA-----GATTAATCAAGTGAAG 653
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 112 PhePhePheGluAspValSerPheProGluAlaSerGluLeuAspGluIlePheLeuGlu 131
QY 654 AAAACCGTAAGAGATCGCTTTTGACACTTTCAGACATACGATGAAGAAGTTCTTAA 713
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 132 ---GlyValGluAsnCysLeuArgAlaPhePheLeuAlaAsp-----LeuAla 147
QY 714 CAAGCTTCAGAGCAGAAAGCTGCTGGAAGATGGGTCCACGTCGATGTTCTGCT 773
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 148 LeuAlaAspAspCysSerIleSerThrSerSerGlyThrAlaLeuThrAlaLeuVal 167
QY 774 GTAGCAACATCTTTATATTCGCAACCTCGAGATAGTCGGCAATCTGTGCTGTA 833
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 168 LeuGlyArgLeuLeuValAlaAsnAlaGlyAspCysArgAlaValLeuCysArgGly 187
QY 834 AATGAGGAAGTCAAAACATGACGCTTAAGCTTACGCAAGAAAGATATCAATCAG 893
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 188 GlyGlu-----AlaIleAspMetSerGlnAspHisArgProThrTyr 201
QY 894 TATGAAGACGATGATGATACAGAGGCTGAGAGAAAGTCCAGGATGGGCGTGTGG 953
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 202 ProSerGluLysArgArgValGluGluLeuGlyGlyTyrValAspAspGlyTyrLeuAsn 221
QY 954 GCGGTGCTAGAGGTGTACGCTTCATTTGGGAGCGGCACTAAG----- 998
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 222 GlyValLeuSerValSerArgAlaLeuGlyAspTyrAspMetLysLeuProLysGlySer 241
QY 999 CGCTGCGGTGTACCTCTGTGCGCCGATCAGACGCTGCAGGTGACCCCAATGACAG 1058
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 242 AlaSerProLeuIleSerGluProGluLeuArgGlnIleIleLeuThrGluAspAspGlu 261
```

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QY 1059 TTCATTTTGTGGCTGTGATGAGGCTCTTCAAGTCTTACCCGAGAAAGCCGTGAC 1118
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 262 PheLeuIleIleGlyCysAspGlyLysThrAspValIleSerSerGlnAlaValSer 281
QY 1119 TTCATCTTGTCTGTCTGTGAGATGAAAGATCCAGACCCGGAGAAAGTCCGACCC 1178
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 282 IleVal-----ArgTyrGlyLeuLysArgHis 290
QY 1179 GAGCCCGCTGACGAGACGCTGCAACAGGCTGCGCAACAGGCGGTGAGGGGCTCG 1238
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 291 AspAspPro---GluGlnSerAlaLysAspLeuValAsnGluAlaLeuArgArgHisThr 309
QY 1239 GCCGACAAAGTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1265
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 310 IleAspAsnLeuThrValIleIleVal 318

RESULT 8
T50783
protein phosphatase 2C-like protein - Arabidopsis thaliana
N:Alternate names: protein T30N20_10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
C:Accession: T50783
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Diskse, W.; Stiekema, W.; Bancroft, I.; New
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25240
A:Accession: T50783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <BEV>
A:Cross-references: EMBL:AL365234
A:Experimental source: cultivar Columbia; BAC clone T30N20
C:Genetics:
A:Map position: 5
A:introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3
A>Note: T30N20_10
C:Superfamily: human phosphoprotein phosphatase 1A

Alignment Scores:
Pred. No.: 1,586-20 Length: 348
Score: 364.50 Matches: 103
Percent Similarity: 53.00% Conservative: 47
Best Local Similarity: 36.40% Mismatches: 86
Query Match: 14.24% Indels: 47
DB: 2 Gaps: 13

US-09-935-124a-1 (1-1422) x T50783 (1-348)
QY 426 GGCATGTGCTGAGCGGAGAGGATGAGAGGAGATGACAGAT---GCCACGTCATC 482
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 35 GlyTyr---AlaSerSerAlaGlyLysArgSerSerMetGluAspPheGluThrArg 53
QY 483 CTGAACGACATCAGCGAGAGGTGAGGCCCCCATGTCCTCATTAATCTCGGTTTCATAT 542
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 54 IleAspGlyIleAsnGlyGluIle-----ValGlyLeu 64
QY 543 TTTGCTGTTTGGATGACATGAGAGAAATTCGAGCTCAAAATTGCTGCACAGAAATTG 602
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 65 PheGlyValPheAspGlyHisGlyGlyValArgAlaAlaGluTyrValLysArgHisLeu 84
QY 603 CATCAAACTTAATCAGAAATTTCTTAAGAGAGATGATACAGTGTGAGAAACCGTG 662
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 85 PheSerAsnLeuIle---ThrHisProLys-----PheIleSer-----AspThr 98
QY 663 AAGAGATGCTTTTGGACATCTTCAAGCATACTGATGAAGATCTCTTAACAGCTTCC 722
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 99 LysSerAlaIleThrAspAlaTyrAsnHisThrAspSerGluLeuLysSerGluAsn 118
QY 723 AGCCGAAGCTGCTGGAAGAT---GGTCCACTGCGACGTGTTCTGCTGTATAC 779
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 119 SerHisAsn-----ArgAspAlaGlySerThrAlaSerThrAlaIleLeuValGly 135
```

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QY 780 AACATCTTTATATGTCACACCTGCGAGATAGTCGGCGCATCTGTCTGTTAATGAG 839
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 136 ABAFARGLLeuValAlaIleAsnValIGlyAspSerArgAlaValIleSerArgGlyGlyAs 155
QY 840 GAGAGTCAAAAACATGACAGCTTAAAGCTTCAGCAAGAGACATATTCACATCAATGAA 899
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 156 -----AlaIleAlaValSerArgAspHisGlyProAspGlnInserAsp 169
QY 900 GAGCGATGAGGATACAGAAAGCTGAGAGAAACGTCAAGGATGGCGCTGTTGGCGGTG 959
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 170 GUAAGGGLuArgILeGluAsnAlaGlyGlyPheVal-----MetTrpAlaGlyVal 186
QY 960 CTAGAGGTGTCAGCTTCATTCATTCGAGCGGCACTAACAAGCTGGCGTACCTCTGAG 1019
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 187 LeuAlaValSerArgAlaPheGlyAspArgLeuLeuGlyGlnTyr---ValValAlaAsp 205
QY 1020 CCGAGATGAGCGCTGTCAGAGTCAAGCAAGAGTTCATTCATTCGCTGAGT 1079
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 206 ProGluILeGlnGluGlyGlyIleAspArgThrLeuGluPheLeuIleLeuAlaSerAsp 225
QY 1080 GGGCTCTTCAGAGTCTTTTACCCCGAAAGAAAGCTGCACTTCATCTGTCTCGAG 1139
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 226 GILYLeuTrpAspValPheSerArgGluAlaValAlaMetVal----- 240
QY 1140 GATGAAAGATCAGACCCGGGAGAGGAGTCCGACCGGACCCCTGACGAAAGACC 1199
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 241 -----LysGluValGluAspPro-----GluAspSer 249
QY 1200 TGCACAGGCTGCGCAACAGCGGTCAGCGGAGCTCGCGGCAACGTCATCTGATGAT 1259
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 250 AlaLysLysLeuValGlyGluAlaIleLysArgGlySerAlaAspAsnIleThrCysVal 269
QY 1260 GTGGTGGCGG 1268
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 270 ValValArg 272

RESULT 9
S54297
Protein phosphatase 2C homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 15-Jun-2001
C:Accession: S54297; T40871
P:Shiozaki, K.; Russell, P.
EMBL J 14, 492-502, 1995
A:Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase hc
A:Reference number: S54297; MUID:95163582; PMID:7859738
A:Accession: S54297
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <SNR>
A:Cross-references: EMBL:L34881; NID:G609655; PIDN:AAA67320.1; PID:G609656
R:Wedler, H.; Wambut, R.; Lyne, M.; Rajandream, M.A.; Barrett, B.G.
Submitted to the EMBL Data Library, September 1998
A:Reference number: Z21953
A:Accession: T40871
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-370 <MED>
A:Cross-references: EMBL:AL031579; PIDN:CAA20880.1; GSPDB:GN00068; SPDB:SPCC1223.11
A:Experimental source: strain 972h-; cosmid c1223
C:Gene: SPCC1223.11
C:Map position: 3
C:Superfamily: human phosphoprotein phosphatase 1A

Alignment Scores:
Pred. No.: 2 57e-20 Length: 370
Score: 362.00 Match: 107
Percent Similarity: 47.68% Conservative: 47
Best Local Similarity: 33.13% Mismatches: 110
Query Match: 14.14% Indels: 59
Db: 2 Gaps: 14

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US-09-935-124a-1 (1-1422) x S54297 (1-370)
QY 407 GGTGATCTTTGGTCTGTAAGGGCTATGTGGCTGAGCGGAGGGTGAAGGAGAGATGCA 466
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 18 GILYAspArgTrp-LeuHisPheGlyValSerHisIleMetGlnGlyTrpArgIleSerMetGln 37
QY 467 GGAATGCCACGTCATCTTCAGAACATCAACCGAG-----GAGTGAAGGCCCCCATGCTC 520
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 37 uAspAlaHisCysAlaLeuLeuAsnPheThrAspSerAsnSerSerAsnProProth- 56
QY 521 CCTGATTAATCGGGTTCATATATTTGCTGTTTGTATGATGACATGAGAAATTCGAGCTC 580
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 57 -----SerPhePheGlyValPheAspGlyHisGlyGlyAspArgValAl 71
QY 581 AAAATTTGTCACAGAAATTTGTCATCAACAACTTAATGAGAAAATTTCT-----AA 631
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 71 alyTrpCysArgGlnIleLeu-----ProAspIleIleLysSerGlnProSerPheTrp 90
QY 632 AGGAGATGTAATACGTGTAGAGAAAACCGTGAAGATGCTTTTGACACTTCAGCA 691
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 90 sGlyAsn-----TyrAspGluAlaLeuLysSerGlyPheLeuAl 103
QY 632 TACTGATGAAGATTCCTTAAACAAAGCTTCAGCGAGAGCTGCGTGAAGATGGCTC 751
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 103 aAlaAspAsnAlaLeuMetGlnAspArgAspMetGlnIuAsp-----ProSerGlyCys 121
QY 752 CACTGCCACGTCGTGTTCTGCTGTAGACAAAC--ATTCTTATATTTGCCAATCTCGAGA 808
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 121 sThrAlaThrThrAlaLeuIleValAspHisGlnValIleTyrCysAlaAsnAlaGlyAs 141
QY 809 TAGTCGGGCAATCTGTGCTGTTATTAAGAGAGAGTCAAAAACATGACAGCTTAAGCTT 868
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 141 pSerArgThrValLeuGlyArg-----LysGlyThrAlaGluProLe 155
QY 869 CAGCAAGAGCATATATCCAACTCAGTATGAGAGCGGATGAGATCAGAAAGCTGAGAG 928
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 155 uSerPheAspHisLysPheAsnAsnAspValGlyLysAlaArgIleThrAlaIleGly 175
QY 929 AAAGGTGAGGATAGGCGGTGTTTGGCGCTGCTAGAGGTGTACGCTCATTCGGGAGAG 988
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 175 yPheIleAspPheGlyArgValAsnGlySerLeuAlaLeuSerArgAlaIleGlyAspPh 195
QY 989 GCAATCAACAGCGTCGGGT-----GTACCTCTGTGCCGA 1024
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 195 eGluTrpLysLysAspSerSerLeuProAspGluLysGlnIleValThrAlaPheProAs 215
QY 1025 CATCAGAGCTGCGACAGTACCCCAATGACAGGTTCAATTTTGGCTGTGATGGCT 1084
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 215 pValAlaIleHisAsnIleAspPheAspAspGluPheLeuIleLeuAlaCysAspGlyI 235
QY 1085 CTTCAAGCTCTTATCCCGAGAAAGAGCCGTAACTTCATCTTGTCTGTCAGAGATGA 1144
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 235 eTrpAspCysLysSerSerGlnGlnValValGluPheVal----- 248
QY 1145 AAAGATCAAGACCCGGGAGAGGAAAGTCCGACGCGGACCGCTACAGACAGCTGCA 1204
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 249 -----ArgArgGlyIleValAlaIaArgInser---LeuGluValIleCysGln 263
QY 1205 CAGGTGCGCAACAGCGGTCAGCGGGGCTG-----GCCGAGAA 1246
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 263 uAsnLeuMetAspArgCysIleAlaSerAsnSerGlnSerCysGlyIleGlyCysAspAs 283
QY 1247 CGTCACTGATGATGTCGTGTCGATAGGCACTAGAGGGGTGCGCGCGACAGACAGC 1306
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 283 nMetThrIleCysIleValAlaPheLeuHis-----GlyArgGlyLeuGluAsp-- 299
QY 1307 ATGTGAT 1313
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 300 -TrpTrp 301

RESULT 10
H96700
protein F12A21.5 [imported] - Arabidopsis thaliana

```

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96700
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Mafti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Author: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96700
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-464 <STO>
 A:Cross-References: GB:A8005173; NID:g11072032; PIDN:AMG28911.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F12A21.5
 A:Map position: 1

Alignment Scores:
 Pred. No.: 2,66e-20 Length: 464
 Score: 362.00 Matches: 108
 Percent Similarity: 45.26% Conservative: 59
 Best Local Similarity: 29.27% Mismatches: 104
 Query Match: 14.14% Indels: 98
 Db: Gaps: 13

US-09-935-124a-1 (1-1422) x H96700 (1-464)

QY 405 TCGGTGATCTTGGTCTGAAGGCTAT---GTGGCTGAGCGAAGGGTGAGGAGGAG 461
 Db 113 ThrValSerPheIleValGlnGlyPheGlyValValSerArgSerMetGlyValSerPhe 132

QY 462 ATGCAGATGCCCGCATCTTGAACGATCAGCAGGAGAGGTGAGGCGCCCATGCTCC 521
 Db 133 MetGluSerPheHisArgIleVal-----ProCysIleValGlyValSer 147

QY 522 CTCATTACTCGGGTTCATATTGCTGTTTGTATGATGACATGAGCAATTCGAGCTCA 581
 Db 148 -----LysIleSerPhePheGlyValTyAspGlyHisIleGlyValAlaValAla 164

QY 582 AATTGTCGCAGAAATTTGATCAAACTTAATGAGAAATTTCT-----AAAGA 635
 Db 165 GluPheValAlaGluIleuSerHisIleValTyValValGluMetCysIleVal 184

QY 636 GATGTATCATGTGTAGAGAAACCGTAGAGATGCTTTTGACACTTTCAAGCATACT 695
 Db 185 LysGluGluLysValGlu-----AlaPheLysAlaIlePheLeuArgThr 199

QY 696 GATGAAGAGTCTTAAACAGAGCTCCAGCCAGAGCCTGCTGGAAGAAGTGGCTCACT 755
 Db 200 AspArgAspPheLeuIleValIleLysGluGlnSerIleValValSerGly 219

QY 756 GCCACGTGTCTGGCTGA-----GACAATCTTTATATTCGCAACTCGGAGAT 809
 Db 220 AlaCysCysValThrAlaValIleGlnIlePheGlnIleValSerHisLeuGlyAsp 239

QY 810 AGTCGGGCAATCTTGTGCTGTTATATGAGAGAGTCAAAAACATGACGCTTAAGCTC 869
 Db 240 CysArgAlaValLeuValSerArgIleGly-----ValAlaGluAlaLeu 253

QY 870 AGCAAAAGACATATCAACTCATGTATGAGAGCGGATGAGATACAGAG----- 920
 Db 254 ThrAspAspHisIleValSerGlyArgAspArgGluValGluIleGluSerIleVal 273

QY 921 -----GCTGAGGAAAGCTCAGGAT-----GGG 944
 Db 274 IleProPheMetThrPheGlyLeuGlnGlyTyValValAspAsnHisGlnGlyAlaTyr 293

QY 945 CGTGTGTTGGCGGTCTAGAGGTGTACGCTTCATTGGGGAGCGGAGTACAAAGCGCTGC 1004
 Db 294 ArgValGlnGlyIleLeuAlaValSerHisSerIleGlyAspAlaHisIleuValSerLys--- 312

QY 1005 GGTGTCACTCTGTGCTCCGACATCAGAGCGCTGACCGCCCAATGACAGTTCATT 1064
 Db 313 TrpValValAlaGluProGluThrArgValLeuGluIleuGluIleuMetGluPheLeu 332

QY 1065 TTGTTGGCGCTGATGAGGCTCTTCAAGCTCTTACCCAGAAAGAGCGGTGAATTCATC 1124
 Db 333 ValLeuAlaSerAspGlyLeuTrpAspValValSerAlaGlnGluAlaValTyThrVal 352

QY 1125 TTGCTCTGCTC-----GAGCATGAAAAATCCAG 1154
 Db 353 LeuHisValLeuAlaGlnArgThrProLysGluSerGluGlnGluIleuValGln 372

QY 1155 -----ACCGGGAAGGG 1166
 Db 373 GlyPheValAsnMetSerProSerSerLysLeuArgAlaSerLeuValLysSerPro 392

QY 1167 AGTCCGCGAGCGGCGCCGCTAC----- 1190
 Db 393 ArgCysAlaLysSerGlnSerIleTyTyThrAsnSerGluAsnGluSerProSerLeuAsn 412

QY 1190 ----- 1190
 Db 413 ArgGluIleGlySerSerProSerLysSerProIleThrProTyLysSerLeuTrpAla 432

QY 1191 GAAAGCACTCTGACAAAGCTGCGCCAAAGCGGTGACAGCGGGCTCGGCGCAACAGC 1250
 Db 433 LysAlaAlaCysLysGluLeuAlaAsnLeuAlaLysArgLysGlySerMetAspAspIle 452

QY 1251 ACTGTGATGTGTGTCGATGAGGCAC 1277
 Db 453 ThrValValIleIleIleAspLeuAsnHis 461

RESULT 11

T00750

probable protein phosphatase 2C [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T20B5.6

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001

C:Accession: T00750; G84834

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, November 1997

A:Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.

A:Reference number: Z14159

A:Accession: T00750

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-404 <ROU>

A:Cross-References: EMBL:AC002409; NID:g2623294; PID:g2623300

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.

ues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617157

A:Accession: G84834

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-404 <STO>

A:Cross-References: GB:A8002093; NID:g2623300; PIDN:AB86446.1; GSPDB:GN00139

A:Gene: T20B5.6; At2g40860

A:Map position: 2

A:Introns: 178/1; 200/2; 273/3; 308/3; 340/3

Alignment Scores:

Pred. No.: 3.37e-20 Length: 404
 Score: 360.50 Matches: 127
 Percent Similarity: 41.82% Conservative: 57

Best Local Similarity: 28.86% Mismatches: 137
 Query Match: 14.08% Indels: 119
 DB: 2 Gaps: 17

US-09-935-124a-1 (1-1422) x T00750 (1-404)

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QY 84 CTCAC---CCAGCTCCGACATGACCTTTCGGGACCTCCGAGCCGAGCCGAC 140
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 26 LeuH1leuProlyserLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 45
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 141 CCGCGCCCGCTGCC----- 155
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 46 LysArgProSerSerAspAsnValValLeuGluLeuGluSerLeuTrpGluGlnValArg 65
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 156 GGGAAAGAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCGGACGAGACT 215
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 66 GlyLys-----GlnGlnGlyLeuLeuGlnGlyLeuSerLeuSerLeuSerLeu 83
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 216 GACTCAGATCAGGGGACCTTTCGCTTTGATGATCCGACCGGCTAGGAGTGGAT 275
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 84 Asp-----GlyAlaAspIleIle-----LysAsnSerGlyAsp 94
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 276 TCAGCTCTCTCCACATCAATCCGACATGTAAGATGAAAGGAAAGAGCAAAAG 335
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 95 TyrArgAspThrValAsnTrpPheSerGln-----GlyGluCysLeuSer 109
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 336 AGAAAACCTCCGAGAAAGAGAGATGGCAGTGAAGCTTGGAAAAGAAAGTTTGT 395
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 110 LysLysSerSer----- 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 396 AAGCCTCTTCGGTATCTTGTCTGAAGGCTATGCTGACCGGAG----- 446
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 114 -----ValSerThrValPheAspValLysLeuTrpSerSerSerThrAspGluProSer 131
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 464
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 132 ArgGlyValProValIleSerCysGlySerPheAlaThrCysGlyValArgGluSerMet 151
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 465 CAGATGATCCGACATGCTGACATGACATGACATGACATGACATGACATGACATG 524
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 152 GluAspThrHisPheIleIleProHISMetCysAsnGlu----- 164
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 525 ATTAGCTGGGTTTCATATTGCTGTTTGTGATGACGATGACGAGAAATTCGAGCTCAAA 584
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 165 ---GluSerIleHisLeuPheHisIlePheAspGlyHisArgGlyAlaAlaAlaGlu 183
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 585 TTTCGTCACAGATTTGTCATCAAAACTTAAATTCGAAATTTCCCTAAAGAGATGATC 644
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 184 PheSerHisGlnValLeu-----ProGlyLeuValGln 194
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 645 AGCTGACAGAAACC---GTGAGAGATGCTTTTGCACATTTGACATGATGATGAA 701
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 195 SerLeuCysSerThrSerAlaGlyAlaLeuSerGlnAlaPheValArgThrAspLeu 214
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 702 GAGTTCCTTAAACAAGCTTCCAGCCAGAACCTGCC-----TGG 740
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 215 AlaPheArgGlnGluLeuAspSerHisArgGlnSerLysArgValSerGlnLysAspTrp 234
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 741 AAGATGGCTCAGCTGACGACGCTGTTCTGCTGTAAGACATTTTATATATGCCAAC 800
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 235 HisProGlyCysThrAlaIleAlaSerLeuLeuValGluAsnLysLeuPheValAlaAsn 254
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 801 CTCGAGATAGTCGGGCAATCTGTGCTGTTATATGAGAGAGAGCAAAAACATGCAGCC 860
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 255 ValGlyAspSerArgAlaIleLeuCysArgAlaGlyHis-----Pro 268
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 861 TTAAAGCTCAGCAAGAGATATCAATCAATCAGTATGAGAGCCGATGAGATCAGAG 920
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 269 PheAlaLeuSerLysAlaHisLeuAlaThrCysIleAspGluAspGlnValIleGly 288
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 921 GCTGAGAGAAAGCTCAGG-----GATGGCGTGTGTTGGCGGTG---CTAGAG 965
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 289 GluGlyGlyArgIleGluTrpLeuValAspThrTrpArgValAlaProAlaGlyLeuGln 308
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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QY 966 GGTTCACGCTTCATTTGGGAGCGGAGCATGACAGCGCTCGGCTGTCACCTCTGTGCCGAC 1025
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 309 ValHisArgSerIleGlyLysAspAspLeuLysPro---AlaValThrAlaGluProGlu 327
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1026 ATCAGACGCTGACGCTGACCCCAATGACAGGTTCAATTTTGGCTGTGATGGCTC 1085
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 328 IleSerIleThrIleLeuSerAlaAspAspGluPheLeuValMetAlaSerAspGlyLeu 347
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1086 TTCAAGGCTCTTACCCCAAGAGAGCCGTGAATCTTCTGCTGCTCGAGAGTAA 1145
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 348 TrpAspValMetAspAspGluGluValIleGlyIleLeuArgAspThrValLysGluPro 367
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1146 AAGATCCAGACCCGAGAGAGAGATGCCAGCCGACGCCGCTAGAGACAGCTGCAC 1205
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 368 SerMetCysSerLys----- 372
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1206 AGGCTGTCACAAAGAGCGGTGACGCGGCTCGGCGGACAGATCATGTATGATGGTG 1265
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 373 ArgLeuAlaThrGluAlaAlaAlaArgGlySerGlyAspAsnIleThrValIleValVal 392
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
 T45778
 Protein phosphatase 2C-like protein - Arabidopsis thaliana
 N:Alternate names: protein P26013.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_rev1sion 04-Feb-2000 #text_change 03-Jun-2002
 C:Accession: T45778
 R:Deisemy, M.; Berger, C.; Cooke, R.; Grelliec, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23013
 A:Accession: T45778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361
 A:Cross-references: EMBL:AL13452
 A:Experimental source: cultivar Columbia; BAC clone P26013
 C:Genetics:
 A:Map position: 3
 A:Introns: 49/3; 108/3
 A:Note: P26013.110
 C:Superfamily: Arabidopsis thaliana hypothetical protein P7A7.220

Alignment Scores:
 Pred. No.: 4,71e-20 Length: 361
 Score: 358.50 Matches: 86
 Percent Similarity: 51.25% Conservative: 58
 Best Local Similarity: 30.60% Mismatches: 96
 Query Match: 14.00% Indels: 41
 DB: 2 Gaps: 8

US-09-935-124a-1 (1-1422) x T45778 (1-361)

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QY 444 AAGGTGAGAGGAGAGATGACGATGCCAGCTCACTCAAGACATCACCGAGAG 503
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 79 LysGlyProLysGlnSerMetGluAspGluPheIleCysValAspAspLeuThrGlyTr 98
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 504 TGTAGGCCCCCATCGCTCATTTACTCGGGTTTCATATTGCTGTTTGTATGACAT 563
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 99 IleGlySerSerThrGly-----AlaPheThrGlyValPheAspGlyHis 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 564 GAGAGATTCGACGCTCAAAATTTGCTGACAGATTTGCGATCAAAACTTAATC----- 617
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 114 GlyGlyValAspAlaHisSerPheThrLysLysAsnIleMetLysLeuValMetGluAsp 133
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 618 AGAAATTTCTTAAAGAGATGTATCAGTGTAGAGAAACCGTGAAGAGATGCTTTTG 677
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 134 LysHisPhePro-----ThSerThrLysValAlaThrArg 145
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 678 GACACTTTCAGAGATCATGATGAAGATTCCTTAAACAGACTTCGACAAAGCTTCGCC 737
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 146 SerAlaPheValLysThrAspHisAlaLeuAlaAspAlaSerSerLeuAspArg----- 163
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Db 315 ThrGlyGluGlyCysAspAsnMetThrIleIleLeuValGln 328

RESULT 14

T04263

Phosphoprotein phosphatase (EC 3.1.3.16) ABI1 - Arabidopsis thaliana

N/Alternate names: protein F20B18.190

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999

C/Accession: T04263; A54588

R/Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohenseil, J.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, March 1999

A/Reference number: Z15263

A/Accession: T04263

A/Molecule type: DNA

A/Residues: 1-434 <REV>

A/Cross-references: EMBL:AL049483

A/Experimental source: cultivar Columbia; BAC clone F20B18

R/Meyer, K.; Leude, M.P.; Groll, E.

Science 264, 1452-1455, 1994

A/Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis th

A/Reference number: A54588; MUID:9425767; PMID:8197457

A/Accession: A54588

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104, 'V', 106-434 <MEV>

A/Cross-references: GB:X78886; NID:G509418; PIDN:CAAS5484.1; PID:G509419

C/Genetics:

A/Map position: 4

A/Introns: 183/3; 280/3; 316/1

A/Note: F20B18.190

C/Keywords: phosphoric monoester hydrolase

Alignment Scores:

Pred. No.:	1,46e-19	Length:	434
Score:	352.50	Matches:	125
Percent Similarity:	44.71%	Conservative:	65
Best local similarity:	29.41%	Mismatches:	148
Query Match:	13.77%	Indels:	87
DB:	2	Gaps:	19

US-09-935-124a-1 (1-1422) x T04263 (1-434)

QY 105 GACCTCTGGGGGACCTTCGCGAGCCCGGAGCGC--TCGCGCGCGCGCGCTCGCGGAGA 161

Db 45 AspLeuMetValSerLeuProGluThrSerSerCysSerValSerGlySerHisGlySer 64

QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGATGACCTCCCGCGCAGCAGTACTGACTCA 221

Db 65 GluSerArgIysValIleuIleSerArgIleAsnSerProAsnLeuAsnMetIysGluSer 84

QY 222 GGATCAGGGGACCTTTCCTTTGATGATCTCCACCGCAGTACGATGGCGAT----- 275

Db 85 AlaIleAlaAspIleValIleValIleValIle-----IleSerIleGlyAspGluIle 100

QY 276 TCAGTTCTCTTCGACATTCATCCAGATGATA--AAGACTGAAGGGAAGAGCA 332

Db 101 AenGlySerAspIleThrSerGluIleValMetIleSerArgThrGlu----- 116

QY 333 AAGAGAAAACCTCCGAGAGAGAAAGATGCGAGTGAAGTCTGTGAGAAAGATT 392

Db 117 -----SerArgSerLeuPheGluPheIys--- 124

QY 393 TGTAAAGCTCTTCGATATTGTTGCTCTAAGGCTATGTGGCTGAGCGAAGGCTGAG 452

Db 125 -----SerValProLeuArgIlePheThrSerIleCys-----GlyArg 137

QY 453 AGGAGAGATGACGATGCGCAGTCATCTTGAACGACATCAACGAGAGTGAAGCCC 512

Db 138 ArgProGluMetGluAspAla-----ValSerThrIleProArgPheLeuGlnSer 154

QY 513 CCAATGCTCCATTT-----ACTGGGTTTCAATATTTCCT 548

Db 155 SerSerGlySerMetLeuAspGlyArgPheAspProGlnSerAlaIlePheAspGly 174

QY 549 GTTTTATGATGACATGAGGAATTCGAGCCCTCAAAAATTGCTGCACAGAAATTGCATCA 608

Db 175 ValIysAspGlyHisGlyGlySerGlnValAlaAsnIleCysArgIleGluArgMetHisLeu 194

QY 609 AACTTATTCAGAAATTTCTTAA-----GGAGATGTAATCAGT 647

Db 195 AlaLeuIleGluIleIleAlaIleGlySerProMetLeuCysAspGlyAspThr---Trp 213

QY 648 GTACAGAAAACCGTAGAAGATGCTTTTGACACCTTTCAGAGATCTCATGAGAGATTC 707

Db 214 LeuIleIysTrp---LysIleValAlaLeuPheAsnSerPheLeuArgValAspSerGluIle 232

QY 708 CTTAAACAAGCTTCACCGCAGAGCTCCGAGAAAGATGGGCTCCACCGCTGCTT 767

Db 233 GluSerValAlaProGluThrVal-----GlySerThrSerValValAla 247

QY 768 CTGCGCTTACAGCAATCTTTATATTCGCCAACCCTGAGATATGTCGGCAATCTGTGT 827

Db 248 ValAlaPheProSerHisIlePheValAlaAsnIleGlyAspSerArgIleValAlaLeuCys 267

QY 828 CATTATATGAGAGAGTCAAAAACATGCACGCTTAAAGCTTCAGCAAGAGCATATATCA 887

Db 268 Arg-----GlyLysThrAlaLeuProLeuSerValAspHisLysPro 281

QY 888 ACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAAACGTC-----AGG 938

Db 282 AspArgGluAspGluAlaIleArgIleGluIleAlaIleGlyGlyValIleGlnTrpAsn 301

QY 939 GATGGCGGTGTTTGGCGCTGATGAGGTGCACGCTCCATTTGGAGCGGACGATGACAG 998

Db 302 GlyAlaArgValAlaPheGlyValIleuIleMetSerArgSerIleGlyAsp---ArgIleu 320

QY 999 CGCTGGCGGTGCACCTGTGCGCCGACATCAGACGCTGACGCGTCAAGCCCAATGACAG 1058

Db 331 LysProSerIleIleProAspProGluValThrAlaValLysArgValIleGluAsp 340

QY 1059 TTCAATTTTGTGGCTGTGATAGGCTCTTCAAGCTTTTACCCGAGAAAGCGTGAAC 1118

Db 341 CysLeuIleLeuAlaSerAspGlyValIleTrpAspValMetThrAspGluIleGlySerIu 360

QY 1119 TTCATC-----TGTGCC 1130

Db 361 MetAlaArgLysArgIleLeuLeuTrpHisLysLysAsnAlaValAlaGlyAspAlaSer 380

QY 1131 TGTCTGAGAGTGAAGATCCAGACCGGAGAGGAAGTCCGACGCGCGCTAC 1190

Db 381 LeuLeuAlaAspGluArg-----ArgLysGluIleLys-----AspProAlaAla 395

QY 1191 GAACGACCTGCAACAGGCTGCGCAACAGGCGGTGACGCGGCTGCGCCACACGCTC 1250

Db 396 MetSerAlaIleGluTrpLeuSerIleLeuAlaIleGlnArgIleSerLysAspAsnIle 415

QY 1251 ACTGTAGTGGTGGTG 1265

Db 416 SerValValValVal 420

RESULT 15

F84650

Probable protein phosphatase 2C (imported) - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002

C/Accession: F84650

R/Klin, X.; Kaul, S.; Rounseley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayam, L.; Tallon, L.;

Nature 402, 761-769, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: F84650

A/Status: preliminary

A/Molecule type: DNA


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Db 90 -LeuSerIleProValAla-----ProValGlyIleAlaAlaProIleSerIleAl 106
QY 248 TGAATCCCAAGCCGCTAGCAGTGCATTCAGGTTCTCTTGCCACATCAATATCCAGAT 307
Db 106 AaerThrProArgGluGlu-----SerArgAl 115
QY 308 GGTAAAGACTGAAGGAAGGCAAGAGAAAAACCTCCGAGAGAGAGAAATGGCAG 367
Db 115 aValGluArgGluGluAaerGly----- 122
QY 368 TGAAGAGCTTGGAAGAAAGTTTAAAGCTTTCGGGATCTTGGTCTGAAGG 427
Db 123 -----TyrSerValTyrCysLys----- 128
QY 428 CTATGTGCTGAGCGAAAGGTGAGAGGAGAGATGCAGATGCCACGTATCTCTGAA 487
Db 129 -----ArgGlyLysArgGluAlaMetGluAaerPheSerAlaIleTh 143
QY 488 CGACATCACCGAGAGTGTAGGCCCATGCTCCCTCATTAATCTCGGTTTCATATTTTGC 547
Db 143 rAenLeuGlnGlyAaer-----ProLysGlnAlaIle-----PheG1 155
QY 548 TGTTTTGAATGACATGAGAGAAATTCAGGCTCAAAATTTGCTGCACAGATTTGCATCA 607
Db 155 yValTyrAaerGlyHisGlyGlyProThrAlaAlaGluPheAlaIalysAenLeuCyse 175
QY 608 AAATTAATCAGAAAAATTTCTAAAGAGATGTATC-----AGTGT 649
Db 175 rAenIleLeu-----GlyGluIleValGlyArgAenGluSerLysI1 190
QY 650 AGAGAAACCGTGAAGAGATGCTTTTGACACTTTGACAGCAATCTGTGAAGATGCTT 709
Db 190 eGluGluAlaValLysArgGlyLysLeu-----AlaThrAaerGluPheLe 206
QY 710 TAAACAGAGCTTCACCGAGAGCCTGCTGAAAAGTGGTGTCACTGCCACGTGTGCTT 769
Db 206 ulysGluLysAenVal-----LysGlyLysSerCysValThrAlaLe 221
QY 770 GGCTGTAGCAACATTTCTTATATGTCCAACTCGAGATAGTGGGCAATCTTGTCG 829
Db 221 uIleSerAaerGlyAaenLeuValValAlaAenAlaGlyAaerCysArgAlaValLeu----- 239
QY 830 TTATTAATGAGAGACTCAAAAACATGACGCTTAAAGCTTCAGCAAAAGCATATATCCAC 889
Db 240 -----SerValGlyGlyPheAlaGluAlaLeuThrSerAaerPheIaArgProSe 255
QY 890 TCAGTATGAAGAGCGATGAGATACAGAGCT----- 923
Db 255 rArgAaerAaerGluArgAaenArgIleGluSerValArgIleLeuAlaLysGluValTh 275
QY 924 -----GGAGGAAACGT 934
Db 275 rValArgPheTyrHisAaerTyrMetValLeuIleThrIleIleLeuGlnGlyLysrVa 295
QY 935 CAGGAGT-----GGGCGTGTGTTGGCGCGTGAAGAGGTGCAGCGCTCCATGG 982
Db 295 laaerThrPheAaenSerValITrPArgIleGlnGlySerIleValAlaSerArgGlyIleG1 315
QY 983 GAGCGGAGCATCAAGCCGCTGCGCTGACCTTGTGCGCCGACATCAAGCGCTCCAGCT 1042
Db 315 yAaerAlaHisLeuLysGln---TrpIleIleSerGluProGluIleAenIleLeuArgI1 334
QY 1043 GACCCCAATGACAGCTTATTTTGGCTGTGATGGGCTCTTCAAGGCTTTTAAACCC 1102
Db 334 eAaerProGlnHisGluPheLeuIleLeuAlaSerAaerGlyLeuTrpAaerLysValSerAs 354
QY 1103 AGAAGAAAGCGTGAATTCATCTTGCTCTGAGATGAAGAAATCCAGACCCGGGA 1162
Db 354 nGlnGluAlaValAaerIle-----AlaArgPr 363
QY 1163 AGGAGATCGCGAGCGCGCCGCTACGAA-----GCAGCTGCAACAGGCTGCGCA 1216
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Db 363 opheCysLysGlyThrAaerGlnLysArgLysProLeuLeuAlaCysLysLysLeuValAs 383
QY 1217 CAAGCGGTGCACAGCGGCGTCCGCGCCGCAACATGCTAGTGAATGAGTACCGGATGAGGCA 1276
Db 383 pleuSerValSerArgGlySerLeuAaerAaerPheIleSerValMetLeuIleGlnLeuCyseH1 403
QY 1277 C 1277
Db 403 s 403

RESULT 17
106308
Protein phosphatase 2C homolog F1IC18.60 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C/Accession: T06308
R/By: Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De Maessene, H.W.; Mayer, K.F.X.; Schueller, C.
Submitted to the Protein Sequence Database, April 1999
A/Reference number: Z15589
A/Accession: T06308
A/Molecule type: DNA
A/Residues: 1-357 <BEV>
A/Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F1IC18.60
A/Experimental source: cultivar Columbia; BAC clone F1IC18
C/Genetics:
A/Gene: ATSP:F1IC18.60
A/Map position: 4
A/Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
C/Superfamily: human phosphoprotein phosphatase 1A

Alignment Scores:
Pred. No.: 2,196-19 Length: 357
Score: 350.00 Matches: 95
Percent Similarity: 46.25% Conservative: 52
Best Local Similarity: 26.53% Mismatches: 95
Query Match: 13.67% Indels: 64
DB: Gaps: 11

US-09-935-124A-1 (1-1422) x T06308 (1-357)
QY 432 GTGCGTAGCGGAGAGGTGAGAGGAGAGAGATGAGATGCCAGTCATCTGAAAGAC 491
Db 432 ----- 45
QY 492 ATCACCGAGAGGTGTAGGCCCCCATGCTCCCTCATTAATCGGGTTTCATATTTGCTGTT 551
Db 492 -----AsnThrSerPheLeuGlyVal 55
QY 552 TTGATGACATGAGAGAAATTCAGAGCTCAAAATTTGCTGCACAGAAATTTGCATCAAAAC 611
Db 552 ----- 75
QY 612 TTATATC-----AGAAATATTTCTTAAAGAGAGTGT---ATCAGTGTAGAGAAACGCTG 662
Db 612 ----- 95
QY 663 AAGAGATGCTTTTGACACTTTCAGAGCATTCAGATGAGAGAGTCTTAAACAGCT--- 719
Db 663 -----MetAaerGluMetGlnGlyGlnArgGlyITrPArgGluLeuValAl 113
QY 719 ----- 719
Db 719 ----- 133
QY 720 -----TCCAGCCGAGAGCT---GCCTGG----- 740
Db 720 ----- 153
QY 741 -----AAAGATGGTCCACTGCGCACGTGTGTTCTGAGCTGTGAGACAAATTTCTT 788
Db 741 ----- 173
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Db      124  GUGluAsp----- 126
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Qy      408  GTGATCTTGTGATGAAGGCTAT-----GTGCTGAGCGGAAGGTGAGAGAGAG 461
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           |||:::
Db      127  -----GlyTyrTyrSerValTyrCybelyarGglYarGglYpro 140
           |||:::
           |||:::
Qy      462  ATGCAAGATGCCACGTCATCTGTAAGACATCAAGAGAGAGGTGAGGCCCATCGTCC 521
           |||:::
           |||:::
Db      141  MetGluAspArgTyrPheAlaAlaValAspArgAsnAspSerPglY----- 156
           |||:::
           |||:::
Qy      522  CTCATTAATCTGGGTTTCATATTGCTGTTTGTGATGAGATGAGAGAAATTCAGGCTCA 581
           |||:::
           |||:::
Db      157  -----TyrTyrAsnAlaPhePheGlyValPheAspGlyValGlySerTyrAlaAla 174
           |||:::
           |||:::
Qy      582  AAATTGCTGCACAGATTTGATCAAACTTAATGAGAAATTTCTTAAGA----- 635
           |||:::
           |||:::
Db      175  GLuPheAlaAlaMetAsnLeuGlyAsnAsnIleGluAlaAlaMetAlaSerAlaArgSer 194
           |||:::
           |||:::
Qy      636  -----GATGTAACTAGTGTAGAGAAACCGTGAAGAGATCCTTTGACACTTTCAAG 689
           |||:::
           |||:::
Db      195  GLyGluAspGlyCySerMetGluSerAlaIleArg-----GluGlyTyrIle 210
           |||:::
           |||:::
Qy      690  CATACTGATGAAGATTTCTTAACAAGCTTCCAGCCCAAGGCTGCGGAAGATGGG 749
           |||:::
           |||:::
Db      211  LysThrAspGluAspPheLeuLysGluGlySer-----ArgGlyGly 224
           |||:::
           |||:::
Qy      750  TCCATGCGCACGCTGTCTGTGCTGTAGACAATCTTTATATGCAACTGCAACTCGGAGAT 809
           |||:::
           |||:::
Db      225  AlaCyCyValThrAlaLeuIleSerLysGlyGluLeuAlaValSerAsnAlaGlyAsp 244
           |||:::
           |||:::
Qy      810  AGTGGGCAATCTTGTGTCTTAAATGAGAGAGTCMAAAACATGACAGCTTTAAGCTTC 869
           |||:::
           |||:::
Db      245  CyAspArgAlaValMet-----SerArgGlyGlyThrAlaGluAlaLeu 258
           |||:::
           |||:::
Qy      870  AGCAAGAGCATTAATCCAATCTGTAAGAGAGCATGAGATGATACGAAGCTGAGAGA 929
           |||:::
           |||:::
Db      259  ThrSerAspHisAsnProSerGlnAlaAsnGluLeuLysArgIleGluAlaLeuGlyGly 278
           |||:::
           |||:::
Qy      930  AACGTGAG-----GATGG-----CGTGTGAGCGCTGTAGAGGTCAGGCTCC 977
           |||:::
           |||:::
Db      279  TyrValAspCySerAsnGlyValIleThrArgIleGlnGlyThrLeuAlaValSerHisGly 298
           |||:::
           |||:::
Qy      978  ATTGGGAGCGGAGTACAAAGCGCTCGGTGACCTGTGTGCGGACATCAGACGCTGC 1037
           |||:::
           |||:::
Db      299  IleGlyAsp---ArgTyrLeuLysIleThrValIleAlaGluProGluThrArgThrLeu 317
           |||:::
           |||:::
Qy      1038  CAGCTACCCCAATGACAGGTTCAATTTGTTGGCTGTGATGGGCTTTCAAGGTCCTTT 1097
           |||:::
           |||:::
Db      318  ArgIleLysProGluPheGluPheLeuIleLeuAlaSerAspGlyLeuThrAspLysVal 337
           |||:::
           |||:::
Qy      1098  ACCCGAAGAAGACCGGTAATCTTCTGTC---TGTCGAGAGTGAAGAAAGATCCAG 1154
           |||:::
           |||:::
Db      338  ThrAsnGlnGluAlaValAspValIleArgProTyrCybAlaGlyValGluAsnProMet 357
           |||:::
           |||:::
Qy      1155  ACCCGGAAGGAAGTCCCGAGCGGACGCCCGCTACGAAGACAGCTGTCAACAGGCTGCC 1214
           |||:::
           |||:::
Db      358  ThrLeu-----SerAlaCybLysLysLeuAla 366
           |||:::
           |||:::
Qy      1215  AACAGGCGGTGACGCGGCTGCGCCGACACGTCATGTGATGGTGGCGGAT 1271
           |||:::
           |||:::
Db      367  GLuLeuSerValLysArgGlySerLeuAspAspIleSerLeuIleIleGlnLeu 385
           |||:::
           |||:::
RESULT 21
S22422
phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - rabbit
NAlternate names: magnesium-dependent protein phosphatase 1A; protein serine/threonine
CSpecies: Oryctolagus cuniculus (domestic rabbit)
CDate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #ext_change 15-Jun-2001
CAccession: S22422
RManu: D.J.; Campbell, D.G.; McGowan, C.H.; Cohen, P.T.W.
Biochim. Biophys. Acta 1130, 100-104, 1992
ATitle: Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and comparative

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A:Reference number: S22422; MUID:92182001; PMID:1311954
A:Accession: S22422
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-382 <MAN>
A:Cross-references: GB:S8757; NID:g247166; PIDN:AA821783.1; PID:g247167
C:Superfamily: human phosphoprotein phosphatase 1A
C:Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Alignment Scores:
Pred. No.: 1,366-18 Length: 382
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 48
DB: 2 Gaps: 12

US-09-935-124a-1 (1-1422) x S22422 (1-382)

Qy      417  GGTCTGAAGGCTATGTGCTGAGCGGAAGGTGAGAGAGATGACAGATGCCAC 476
           |||:::
           |||:::
Db      21  GYleuArgTyrGlyLeuSerSerMetGlnGlyThrArgValGluMetGluAspAlaHis 40
           |||:::
           |||:::
Qy      477  GTTATCTGATGACATCAAGAGATGAGAGATGAGGCCCATGCTCCCTCATTAATCTGGGTT 536
           |||:::
           |||:::
Db      41  ThrAlaValIleGlyLeu-----ProserGlyLeuGluThr---Trp 53
           |||:::
           |||:::
Qy      537  TCATATTTTGTGCTTTTGTGCTGAGCGGAAGGTGAGAGATTCGACCTCAAAATTTGCTGCACAG 596
           |||:::
           |||:::
Db      54  SerPhePheAlaValTyrAspGlyHisAlaGlySerGlnValAlaLysTyrCySerGlu 73
           |||:::
           |||:::
Qy      597  AATTGTCATCAAACTTAATCAAAATTTCTCT---AAAGAGAT-----GTAACTAGT 647
           |||:::
           |||:::
Db      74  HisLeuLeuAspHisIleThrAsnAsnGluAspPheLysGlySerAlaGlyAlaProSer 93
           |||:::
           |||:::
Qy      648  GTAGAGAAAACCGTAAGATGCTTTTGGACACTTTCAACAGATCTGATGAAGATTC 707
           |||:::
           |||:::
Db      94  ValGlu---AsnValLysAsnGlyLeuArgThrGlyPheLeuGluIleAspGluHisMet 112
           |||:::
           |||:::
Qy      708  CTTAAACAAGCTCCAGCGCAAGGCTGCGTGAAGATGGGTGACATGCGGACGCTGTGT 767
           |||:::
           |||:::
Db      113  ArgValMetSerGluLysLeuHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
           |||:::
           |||:::
Qy      768  CTGCTGTAGACACATCTTATATGTCACCTCGAGATAGTCGGGCAATCTTGTGT 827
           |||:::
           |||:::
Db      133  LeuIleSerProGlnHisThrTyrPheIleAsnCySerGlyAspSerArgGlyLeuLeuCyS 152
           |||:::
           |||:::
Qy      828  CGTTATTAATGAGAGAGATCAAAACATGACGCTTAAGCTTCAGCAAAAGCATTAATCCA 887
           |||:::
           |||:::
Db      153  Arg-----AsnArgLysValHisPhePheThrGlnAspHisLysPro 166
           |||:::
           |||:::
Qy      888  ACTCAGTATGAAGAGCGGATGAGTACGATCAAGAGCTGAGAGAAAGTCAGAGATGGGCGT 947
           |||:::
           |||:::
Db      167  SerAsnProLeuGlnLysGluArgIleGlnAsnAlaGlyGlySerValMetIleGlnArg 186
           |||:::
           |||:::
Qy      948  GTTTTGCGCTGCTAGAGGTGTCAAGCTCAATTTGGGAGCGGACATCAAGAGCGTGC--- 1004
           |||:::
           |||:::
Db      187  ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
           |||:::
           |||:::
Qy      1005  -----GGTGCACC-----TTGTGCCGACATCAGA 1031
           |||:::
           |||:::
Db      206  HisGlyLysGlyProThrGlnGlnLeuValSerProGluProGluValHisAspIleGlu 225
           |||:::
           |||:::
Qy      1032  CGCTGCCAGCTGACCCCAAGTACAGATTTTGTGCTGAGCGCTGAGAGCTTTCAAG 1091
           |||:::
           |||:::
Db      226  ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCyAspGlyLysLeuAsp 243
           |||:::
           |||:::
Qy      1092  GTCTTATCCCAAGAGAAGCCGTGAATCTTCTGCTGCTGAGAG-----GATGAA 1145
           |||:::
           |||:::
Db      244  ValMetGlyAsnGlnGluLeuCyAspPheValaArgSerArgLeuGluValThrAspAsp 263
           |||:::
           |||:::
Qy      1146  AAGATTCAGACCCGGGAAGGAAGTCCGACGCCGACGCCCGCTACGAAGACGCTTGACAC 1205
           |||:::
           |||:::

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Db 264 -----LeuGluYsValCyAsn 269

Qy 1206 AGGCTGGCCAAAGAGCGGTGACGGGGCTCGGCCGAAGATGACGTGATGCGTG 1265
Db 270 GluValValAspThrCysLeuTrpGlySerArgAspAsmSerValIleLeuIle 289

RESULT 22

A32399
phosphoprotein phosphatase (EC 3.1.3.16) 1A - rat
N/Alternate names: protein phosphatase 2C
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 15-Jun-2001
C/Accession: A32399
R/Tamura, S.; Lynch, K.R.; Larner, J.; Fox, J.; Yasui, A.; Kikuchi, K.; Suzuki, Y.; Tsui
Proc. Natl. Acad. Sci. U.S.A. 86, 1796-1800, 1989
A/Title: Molecular cloning of rat type 2C (1A) protein phosphatase mRNA.
A/Reference number: A32399; MUID:89184515; PMID:2538815
A/Accession: A32399
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-382 <TAM>
A/Cross-references: GB:J04503; NID:9206312; PID:AAA41917.1; PID:9206313
C/Keyword: liver; phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Alignment Scores:

Pred. No.:	1,36e-18	Length:	382
Score:	340.00	Matches:	101
Percent Similarity:	49.33%	Conservative:	47
Best Local Similarity:	33.67%	Mismatches:	104
Query Match:	13.28%	Indels:	48
DB:	2	Gaps:	12

US-09-935-124A-1 (1-1422) x A32399 (1-382)

Qy 417 GGTCTGAAGGCTATGTGGCTGACGGAGCGAGAGAGATGACAGATGCCAC 476
Db 21 GlyLeuArgTrpGlyLeuSerSerMetGlnGlyTPrArgValGluMetGluAspAlaHis 40

Qy 477 GTGATCTGAAAGCATGACAGCGAGAGAGTGAAGCGCCCATCGCTCATATCGGGATT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---Trp 53

Qy 537 TCATATTTGCTGTTTGGATGAGCATGAGAAATTCGCAATTTGCTGCGACAG 596
Db 54 SerPhePheAlaValTrpArgLysIleAlaGlySerGlnValAlaLeuTrpCysGly 73

Qy 597 AATTGTCATCAAACTTAATCAAAAATTCTCT--AAAGAGAT-----GTATCACT 647
Db 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLeuGlySerAlaGlyAlaProSer 93

Qy 648 GTAGAGAAAACCTGAAGAGATGCTTTTGACACATTTCAAGCATATGATGAAGTTT 707
Db 94 ValGlu--AsnValLysAsnGlyIleArgThrGlyPheLeuGluIleAspGlnIleMet 112

Qy 708 CTTAAACAGCTTCCAGCAGAGACCTGCTGGAAGATGGTCCAGTCCACCTGTGTT 767
Db 113 ArgValMetSerGlnLysLeuIleGlyAlaAspArgSerGlySerThrAlaValGlyVal 132

Qy 768 CTGGGTGTAGACACATCTTTATATGTCGCAACCTCGAGATAGTGGGCAATCTGTGT 827
Db 133 LeuIleSerProGlnIleThrTrpPheIleAsnGlyLysAspSerArgGlyLeuLeuCys 152

Qy 828 CGTTATATGAGAGAGATCAAAACATGACAGCCTTAAGCTCAGCAAAAGACATATCC 887
Db 153 Arg-----AsnArgLysValIleHisPheThrGlnAspHisLysPro 166

Qy 888 ACTCAGATATGAGAGCGATAGAGATCAAGAGCTGAGAAAGTCAAGATGGGCGT 947
Db 167 SerAsnProLeuGlnLysGlnArgLysIleAsnAlaGlyLysValMetIleGlnArg 186

Qy 948 GTTTTGGCGTGTAGAGGTCTACGCTCCATGGGGAGCGGACATACAGCGCTGC-- 1004
Db 948 GTTTTGGCGTGTAGAGGTCTACGCTCCATGGGGAGCGGACATACAGCGCTGC-- 1004

Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTrpLys---CysVal 205

Qy 1005 -----GRTGTACC-----TCTGTCCCGGACATCGA 1031
Db 206 HisGlyLysGlyProThrGlnGluLeuValSerProGluProGluValHisAspIleLeu 225

Qy 1032 CGCTGCCAGCTGACCCCCAATGACAGGTTTCATTTGTGGCTGTGATGGCTCTTCAAG 1091
Db 226 ArgSerLys-----GluAspAspGlnPheIleLeuAlaCysAspLysIleTrpAsp 243

Qy 1092 GTCTTTACCCCAAGAGACCCGTGAACCTTCAATCTTGCTGTCTCGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnGluLeuLeuCysAspPheValArgSerArgLeuGluValThrAspAsp 263

Qy 1146 AAGATCCAGACCCGGAGAGGAATGCCAGACCCGCTACGACAGACGCTGCAAC 1205
Db 264 -----LeuGlnLysValCyAsn 269

Qy 1206 AGGCTGGCCAAAGAGCGGTGACGGGGCTCGGCCGAAGATGACGTGATGCGTG 1265
Db 270 GluValValAspThrCysLeuTrpGlySerArgAspAsmSerValIleLeuIle 289

RESULT 23

T48018
hypothetical protein T17013.220 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C/Accession: T48018
R/Rieger, M.; Mueller-Auer, S.; Zilp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A/Reference number: Z24482
A/Accession: T48018
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-383 <RIE>
A/Cross-references: EMBL:AL138651
A/Experimental source: cultivar Columbia; BAC clone T17013
C/Genetics:
A/Map position: 3
A/Introns: 56/3; 118/3; 197/2
A/Note: T17013.220

Alignment Scores:

Pred. No.:	1,78e-18	Length:	383
Score:	338.50	Matches:	108
Percent Similarity:	46.57%	Conservative:	67
Best Local Similarity:	28.12%	Mismatches:	128
Query Match:	13.22%	Indels:	81
DB:	2	Gaps:	15

US-09-935-124A-1 (1-1422) x T48018 (1-383)

Qy 183 CTTTGTGATGACCTCCCTCGGCGCAGATCTGATCAGATCAGGGGACCTTTGCTT 242
Db 21 LeuPheAspLysVal-----SerSerAlaValLysSerProValSerSerProLysLeu 38

Qy 243 TTTGATGATCTCCACCCGCTAGCAGTGGCGGATGACAGTTCTTGTCCACATCATATCC 302
Db 39 -----GlyPheThrGlnSerThrAlaSerValSerLysLeuThrThrSerProVal 56

Qy 303 CAGATGTAAGAAGCTAAGGAGAAAGCAAGAAAGAAAACCTCCGAGAAAGAAAGAT 362
Db 57 AlaAspIlePheProGlnLysAsp----- 64

Qy 363 GGCAGTAAAGCTTTGTGAAAAGAAAGTTTGTAAAGCTCTTCGGTATCTTTGGTGTG 422
Db 65 -----CysAspProSer-----Val 69

Qy 423 AAGGCTATGTGGCTAGCGGAG-----GTCAGAGAGAGAG 461
Db 70 LeuAspTrpIleProThrIleArgSerGlySerPheAlaAspIleGlyProLysArgAsn 89

Qy 462 ATGAGAGATGCCAGATCATCTTAAGACATCACGAGAGATGTAGCCCCCATGTCC 521

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CC      phosphate.
CC      -1- COPOLYMER BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY) .
CC      -1- SUBUNIT: MONOMER.
CC      -1- SIMILARITY: BELONGS TO THE P2PC FAMILY
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
DR      EMBL; L34882; AAA67321.1; -
DR      DDBJ; Z54354; CAA91172.1; -
DR      HSSP; P35813; 1A6O.
DR      InterPro; IPR001932; P2PC-like.
DR      PIR; PIR00222; P2PC.
DR      Pfam; PF00481; P2PC; 1.
DR      SMART; SM00331; P2PC_SIG; 1.
DR      SMART; SM00332; P2PC; 1.
DR      PROSITE; PS01032; P2PC; 1.
KM      Hydroxylase; Magnesium; Manganese; Multigene family.
FT      METAL 37 37 MANGANESE 1 (BY SIMILARITY) .
FT      METAL 38 38 MANGANESE 1 (BY SIMILARITY) .
FT      METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY) .
FT      METAL 230 230 MANGANESE 2 (BY SIMILARITY) .
FT      METAL 239 279 MANGANESE 2 (BY SIMILARITY) .
FT      CONFLICT 196 196 K -> T (IN REF. 1) .
SQ      SEQUENCE 414 AA; 44856 MW; EFP3A416625A2B11 CRC64;
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Score: 380.50 Matches: 111
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Best Local Similarity: 32.46% Mismatches: 105
Query Match: 14.86% Indels: 71
Gaps: 14
US-09-935-124A-1 (1-1422) x P2C3_SCHPO (1-414)
Oy      342 ACCTCGACGAGAAAGAAATGCACTGAGAGAGCTTGCGAAAAAGAAAGTTGTGAAGCC 401
Db      ||| ::| ||||| ||||| |||||
Oy      10 ThGluLyhIsSeVAlaenGlySeRaenGluPhe----- 21
Db      ||| ::| ||||| ||||| |||||
Oy      402 TCTTCGGGATCTTTGGCTTGAAGGGCTATGCGCTGAGCGAAAGGTGAGAGGAGAG 461
Db      22 -----ValLeuTyGLeuLeu-----SerSerMetGInGlyTrpArgLeSer 35
Oy      462 ATGCAGATGCCACGATCTCTGAACGACATCCAGCCAGAGGTGAGAGGCCCATCTGTC 521
Db      ||| ::| ||||| ||||| |||||
Oy      36 MeGluApeRAlaHisSerAlaIle-----LeuSerMetGInGlyCys-----SerAla 50
Db      ||| ::| ||||| ||||| |||||
Oy      522 CTCATTAATCCGGGGTTTCAATATTTGGCTGTTTGAATGACATGAGAGAAATTCAGACCTCA 581
Db      ::| ::| ||||| ||||| ||||| |||||
Oy      51 ValLyAaSPeRAlaHisSerAlaIleValTyGArgGlyHisGlyLeuApeRyValAla 70
Db      ||| ::| ||||| ||||| |||||
Oy      582 AAATTTGGCGACAGAAATTTGCAATCAAAATCTTAATCAAGAAA-----TTTCTTAAGA 635
Db      ::| ::| ||||| ||||| ||||| |||||
Oy      71 LyGTrpCyGlySeRaenLeuProGInIleuGInuLySaPeRCoApeRheGInuLeu 90
Db      ||| ::| ||||| ||||| |||||
Oy      636 GATGTAATAGGTAGAGAAAC-----GTGAAGAGATGCCCTTTGGACACT 683
Db      ||| ::| ||||| ||||| |||||
Oy      91 AaPeRheValaenAlaLeuLySeSerPheLeuAenAlaApeRyAlaIleLeuAaP- 109
Db      ||| ::| ||||| ||||| |||||
Oy      684 TTCAACACATCTGATGAAGAGACTTCTTAAACAGACTTCGACCCAGAAAGCTGCTGGAAA 743
Db      ||| ::| ||||| ||||| |||||
Oy      110 -----AaPeRAlnPhenHisTrpAaPProSer----- 118
Db      ||| ::| ||||| ||||| |||||
Oy      744 GATGGTCACTGCGACGCTGTGTCTTGCGCTGTAGACAAATCTTTATATATGCAACTC 803
Db      ||| ::| ||||| ||||| |||||
Oy      119 ---GlyCvThAlaTrhAlaTrhValaIleuAaGValaIleuAaLyLeuTyCyAlaIaenAla 137

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Qy	804	GGAAGATGCGGGGCAACCTTGTCGCTTATATAGAGAGACTCAAAAACATGACGCTTA	863
Db	138	GIYAsperArghThralValuu-----GlyserlysgIlylIeAlAsy	151
Qy	864	AGCCTCAGGAAMAGSCATTATCCAACTCAGTGTGMAAGACCGAGAGAGATACGAAGGCT	923
Db	152	ProteinSerAlaephylslyPProSerAengIuAlagIuysAlaAlagIleCySaAlaAla	171
Qy	924	GGAGGAACGTCAGGAGTGGCGGCTGTTTGGCGGTCGTACAGGTGTACGCTTCATTGGG	983
Db	172	GIYGIYPheValaAsPhehGlyAhsValaIsengIyAlaenIAlaIsenSerAgaAlaIleGly	191
Qy	984	GACGGCAGTACAGACGCGTGCGGT-----GTCACTCTGTGCC	1022
Db	192	AsPhehGluPheIyAAsenSerAenIuPProGluIySgInIleValThralAlaIeuPto	211
Qy	1023	GACATCAGACGCGTGCACGACTGACCCCAATGACAGGTTCAATTTGTGTGCGCTGTATGGG	1082
Db	212	AspValaIvalAlaHsguIleThralAspAAspAAspGluPheValaIleuAlaIaCySaAspGly	231
Qy	1083	CTCTTAAAGTCTTTTACCCCAAGAAAGCGCGGAACCTTCATCTTGTCCTGTCTCGAGAT	1142
Db	232	IlleTAspCyIyThrsSerGInGInValIleGluPheVal-----	245
Qy	1143	GAAMAATCAGACCCCGGGAAGGAAGTCCGACGCCAGCGCCGCTACGAAGCAGCC--	1199
Db	246	-----ArgAsgIlylIleValAlaIagIyThrsIerIeIuGluIySAlaIagIu	260
Qy	1200	-----TGCAACAGCGCTGGCGCAACGAAGGGGGrTCAGCGCGGCG--TCGCGCGCAAC	1247
Db	261	AsnIeMeIeAsPhehGlySAlleAlaIserAAspThrgIuThrIrgIyIeIuGlySAspAAspAn	280
Qy	1248	GTCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1307
Db	281	MeThIValaCySAlleValAlaIeu-----LeuGInGluAAsnAAspIySserAla	296
Qy	1308	TGGTAT 1313	
Db	297	TriPtyr 298	
RESULT 3			
P2C2	SCHPO	STANDARD;	PRT; 370 AA.
ID	P2C2_SCHPO		
AC	009172;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).		
GN	PP2C OR SPCC1223.11.		
OS	Schizosaccharomyces pombe (fission yeast).		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;		
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;		
OC	Schizosaccharomycetes.		
OX	NCBI_TaxID=4896;		
NN	[1]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=972.		
RC	MEDLINE=95161582; PubMed=7859738;		
RA	Shiozaki K., Ruseell P.,		
RT	"Counteractive roles of protein phosphatase 2C (PP2C) and a MAP		
RT	kinase kinase homolog in the osmoregulation of fission yeast."		
RL	EMBO J. 14:492-502(1995).		
RU	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=972.		
RC	MEDLINE=21648401; PubMed=11859360;		
RA	Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,		
RA	Sbours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,		
RA	Brooks K., Brown D., Brown S., Chillingworth I., Churcher C.W.,		
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,		
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,		
RA	Holmoyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsla J.,		
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,		

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Stammers M., Squares R., Stevens S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambolt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Laureau V., Motier S.,
 RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garçon A., Thode G.,
 RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Pothakkin J.,
 RA Shpakovski G.V., Usero D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
 CC SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
 CC TRANSMITTED THROUGH WISKI MAP KINASE.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 DR EMBL, L34881, AA67320.1, -.
 DR EMBL, AL031579, CA20880.1, -.
 DR HSSP, P35813, IAOQ.
 DR InterPro, IPR001932, PP2C-like.
 DR InterPro, IPR00222, PP2C.
 DR Pfam, PF00481, PP2C_1.
 DR SMART, SM00331, PP2C_Sig_1.
 DR SMART, SM00332, PP2C_1.
 DR PROSITE, PS01032, PP2C; 1.
 DR HydroLase; Magnesium; Manganese; Multigene family.
 KW METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 63 63 MANGANESE 2 (BY SIMILARITY).
 FT METAL 233 233 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 370 AA; 40878 MW; DBDDB826F440AC50 CRC64;
 Alignment Scores:
 Pred. No.: 1.4e-18 Length: 370
 Score: 362.00 Matches: 107
 Percent Similarity: 47.68% Conservative: 47
 Best Local Similarity: 33.13% Mismatches: 110
 Query Match: 14.14% Indels: 59
 DB: 1 Gaps: 14
 US-09-935-124a-1 (1-1422) x P2C2_SCHPO (1-370)
 QY 407 GGATGATCTTGGTGTGAAGGCGATGTGAGCGAGGTGAAGAGGAGAGATGCA 466
 DB 18 GtAaBpAgtGtP-LeuHlaPheGlyValSerHlmeGInGlyTPHAgylIsSerMeGcl 37
 QY 467 GGATGCCCAAGTCATCTGAGACATCAACGAGGAGGATGAGCGCCCATGTC 520
 DB 37 uAePrlaHlScyBaLaLeuHlaAnPheHlraPseRlaSenSerAaPPrIoThr-- 56
 QY 521 CCTCATCTACGGGTTTCATATTTGCTTTTGTGATGACATGAGGAATTCGAGCCTC 580

DB 57 -----SerPhePheGlyValPheAspGlyHlGlyGlyAaPrgValAl 71
 QY 581 AAAATTTCTGCACAGAAATTTGCATCAAACTTATCATGAAATTTCT--AA 631
 DB 71 alyeYrCySaRgInHlSleu---ProAsPrllellelySerGlnProSerPheTrpLy 90
 QY 632 AGGAGATGTAATCACTGTAGAGAAAACCTGAGAGATGCTTTTGGACACTTTGACA 691
 DB 90 gGlyAaH-----TyrAsPrluAlaLeuHlySerGlyPheLeuAl 103
 QY 692 TACTGATGAAGTTCCTTAAACAAGTTCACAGAGAGCTGCGTGAAGAAGTGGTC 751
 DB 103 aAlaPhePnaAlaLeuWeGlnAsPrgAsPmeGlnuAsP-----ProSerGlyCy 121
 QY 752 CACTGCCACGTGTGTTCTGAGTGTAGAAC--ATTCTTATATATGCCAATTCGAGAGA 808
 DB 121 eThrlaHlThrlaLeuAlleValaAsPrlGlnValleYrCySaLaBnaAlaGlyAs 141
 QY 809 TAGTGGGCAATCTTGTGCTGTATATGAGAGAGTCAAAACAATGACGCTTAAGCT 868
 DB 141 pSerArGThrValleuGlyArg-----LysGlyThrlaGluProLe 155
 QY 869 CAGCAAGAAGCATATCAACTCAGTATGAGAGCGGATGAGATACAGAGGCTGAGG 928
 DB 155 userPheAsPrlslyPProaBnaBnaPrgValGlnuYsaLaRgylleThrlaAlaGlyG 175
 QY 929 AAACGTCAAGATGGCGCTGTTTGGCGCTGACAGGTGTACAGCTTCATTTGGAGAGCG 988
 DB 175 yPheHlaPhePheGlyArgValaGlnGlySerLeuHlaLeuSerArGAlleGlyAsPrl 195
 QY 989 GCAGTACAGAGCTGCGGT-----GTACCTCTGTGCCCCGA 1024
 DB 195 eGlnuYrlyrlySlyAsPseSerleuProGlnuYsGlnlleValThrlaAlaPheProAs 215
 QY 1025 CATCAAGAGCGTCCAGACGCCCAATGACAGAGTTCATTTGTTGGCTGTGATGGCT 1084
 DB 215 pValaValleHlSleuHlAsPrlAsPrgAsPrgGlnuPheulleuAlaCySaAsPrlYl 235
 QY 1085 CTTCAAGGCTTTTACCCCAAGAAAGCCGTGAATTCATTTGTCCTGTCGAGATGA 1144
 DB 235 eTrpAsPrgCySlySseSerGlnGlnValaGlnuPheVal----- 248
 QY 1145 AAAGATCCAGACCCGGAAGGAAAGTCCGACGCGAGCGCCGCTACGAGACCTGCA 1204
 DB 249 -----ArgArGlylleValaAlaArgGlnSer---LeuGlnuAlleleCyGcl 263
 QY 1205 CAGGTGGCCAACAAGCGGTCGACGCGGCTCG-----GCCGACAA 1246
 DB 263 uAsnleuHlscPArGlyCyHlAlaSerAaSenSerGlnuCySlyGlyCySaAsPrg 283
 QY 1247 GGTCACTGTGATGTGTGCGGATAGGACACTGAGAGGAGTGGCGCGGCGAGAGCAGCG 1306
 DB 283 nMeThrlleCySlylleValaAlaPheLeuHlS-----GlyArGlnGlyLeuGluAsP-- 299
 QY 1307 ATGGTAT 1313
 DB 300 -TrpTyR 301
 RESULT 4
 ID FEM2_HUMAN STANDARD; PRT; 454 AA.
 AC P49593; Q96PM2;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
 DE (CamKpase) (hFEM-2).
 GN KIAA0015.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
RX PubMed=11559703;
RA Tan K.M.L., Chan S.L., Tan K.O., Yu V.C.;
RT "The Caenorhabditis elegans sex-determining protein fem-2 and its
RT human homologue, hFEM-2, are Ca2+/calmodulin-dependent protein kinase
RT phosphatases that promote apoptosis.",
RL J. Biol. Chem. 276:44193-44202(2001).
RN [2].
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki T., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K14A0001-K14A0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RL DNA Res. 1:27-35(1994).
CC -1- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
CC kinase II activated upon autophosphorylation, and Cam-kinases IV
CC and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: Associates with FlapApha.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL; AF305840; AAL15579.1; -;
DR EMBL; D13640; BAA02803.1; -;
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR002222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KM Hydroxylase; Magnesium; Apoptosis; Multigene family.
FT DOMAIN 101 107 POLY-GLU.
FT METAL 360 360 MANGANESE 2 (BY SIMILARITY).
FT METAL 404 404 MANGANESE 2 (BY SIMILARITY).
FT CONFLICT 202 202 D -> G (IN REF. 2).
SQ SEQUENCE 454 AA; 43988 MW; 2A56263331BC9CF CRC64;

Alignment Scores:
Pred. No.: 2, 23e-18 Length: 454
Score: 359.50 Matches: 126
Percent Similarity: 42.63% Conservative: 65
Best Local Similarity: 28.12% Mismatches: 146
Query Match: 14.04% Indels: 111
DB: 1 Gaps: 16

US-09-935-124A-1 (1-1422) x FEM2_HUMAN (1-454)
QY 129 CCCGAGCGCTGCGCGCGCGCTGCGCGGAAAAGACTGAAAAGACCCCTG----- 182
DB 6 ProGlnlySerSerPromeAlaSerGlyAlaGlnGluThrProGlyPheLeuAsePThr 25
QY 183 CTCCTTGTGAGCACTCCCTCCGCGCCAGCAGCAGTGAAGTCAAGATCAGGGGAGCCTTGCTT 242
DB 26 LeuLeuGlnAsePheProAlaLeuLeuAsePProGlu----- 37
QY 243 TTTGATGATCTCCACCGCTAGAGTGGCGAT-----TCAGGT 281
DB 38 ---AseProLeuProThrTplyAlaProGlyThrValLeuSerGlnGluGluValGluGly 56

QY 282 TCTCTGGC----- 290
DB 57 GluLeuAlaGluLeuAlaMetGlyPheLeuGlySerArglyAlaProProProLeuAla 76
QY 291 -----ACATCAATATCCCAAGTGAATGAACATGAA-----GGG 323
DB 77 AlaAlaLeuAlaHleGluAlaValSerLeuLeuLeuGlnThrAspLeuSerGluPheArg 96
QY 324 AAAGAGCAAAAGAAACAACTCCGAGAAAGAGAAAGATGCAAGTGAAGACCTTGAGAA 383
DB 97 LysLeuProArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 116
QY 384 AAGAAATTTGAAAGCTCTTCGATGATCTTGTGTCGAGAGGCTATGAGCTGACCGG 443
DB 117 ValThrLeuLeuAspAlaGlnSerLeuAlaGlnSerPheAsnArgLeuTrpGluVal 136
QY 444 AAGGCTGAG----- 452
DB 137 AlaGlyGlnThrGlnGlnGlnValProLeuAlaAlaArgAlaSerGlnArgGlnTrpLeu 156
QY 453 -----AGGAGAGAGATGACAGATGCCACATGATCTG 485
DB 157 ValSerLeuHleAlaAlaArgAsnThrArgArgGlyMetGluAspArgHleValSerLeu 176
QY 486 AAGACATACACGAGAGAGTGAAGCCCAACGACCTGATTAAGTGGATTGATTTT 545
DB 177 ProSerPhe---AsnGlnLeuPheGlyLeuSerPheProValAsnArg---AlaTyrPhe 194
QY 546 GCTGTTTGTGATGAGCAATGAGAAATTCGAGCTCAAAATTTGCTGTCACAAATTTGAT 605
DB 195 AlaAlaPheSerPlyAlaGlyAlaSerValAspValAspAlaArgValAlaValAlaHle 214
QY 606 CAATATTAATCAAAA-----TTTCTAAAGAGATGTAATCAAGTGA 650
DB 215 ThrAsnAlaAlaArgGlnProGlnLeuProThrAspProGlnGly----- 229
QY 651 GAGAAACCGTGAAGAGATGCTTTTGGACACATTTGAACATATGATGAAGTCTT 710
DB 230 -----AlaLeuAlaGluAlaPheArgArgThrAspGlnMetPheLeu 243
QY 711 AAACAGCTTCCAGCCAGAGAGCTGCTGCGAAAGATGAGTTCACAGCTGTGTTCTT 770
DB 244 ArglyAlaValArgGlnArg-----LeuGlnSerGlyThrThrGlyValCysAlaLeu 261
QY 771 GCTGTAAACAACATCTTATATATGTCACACCTGCGAATATGTCGGAATCTGTGTCGT 830
DB 262 HleAlaGlyAlaThrLeuHleValAlaThrLeuGlyAspSerGlnValHleVal----- 280
QY 831 TATATAGAGAGAGTCAAAACATGACAGCTTAAGCTCAGAGAAAGACATTAATCAACT 890
DB 281 -----GlnGlnGlyGlnValValLeuLeuMetGlnProHleArgProGlu 295
QY 891 CAGATGAGAGCGAGTGAAGTATCAGAAAGCTGAGAGAAAGCTCAGAGAT----- 941
DB 296 ArgGlnAspGlnGlyAlaArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 315
QY 942 GAGCGTGTGTTGGCGGTGCTGAAGGTGTCAAGCTCAATTTGGGAGCGGCACTGACAGCC 1001
DB 316 TrpArgValAsnGlyThrLeuAlaValSerArgAlaHleGlyAsp---ValPheGlnGly 334
QY 1002 TGCGGTGTCACTGTGTGCCGACATCAAGAGCTGCAAGTGAACCCCAATGACAGGTTT 1061
DB 335 ProTyrAlaSerGlyGlyAlaAspAlaAlaSerArgAlaLeuThrGlySerGlnAspTyr 354
QY 1062 ATTTTGTGGCCGTGATGAGCTCTTCAAGTCTTTTAAACCCAGAAAGACCGTGAATTC 1121
DB 355 LeuLeuLeuAlaCysAspGlyPhePheAspValValProHleGlnGlnValValGlyLeu 374
QY 1122 ATCTTGCTGTGTGTCGAGAGTGAAGATGCAAGCTGGAAGAGGAGAAATGTCGCGAGCCGAC 1181
DB 375 ValGlnSerHleLeu-----ThrArgGlnGlnGlySerGlyLeuArg 388
QY 1182 GCCCGCTAGAGAGAGAGCTGCAAGAGCTGCGCAAGAGCGGTGACAGGGGCTCGGCC 1241

DB 389 ValAlaGluGlu-----LeuValAlaAlaAlaArgGluValArgGlySerHis 403
 QY 1242 GACAACGTCATCTGATGCTGCTG 1265
 DB 404 AspaenilleThrValMetValVal 411
 RESULT 5
 P2C1 ARATH STANDARD; PRT; 434 AA.
 AC P49597; Q43717; Q94C87;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein phosphatase 2C AB11 (EC 3.1.3.16) (PP2C) (Abscisic acid-insensitive 1).
 GN AB11 OR AT4G26080 OR F20B18.190.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=94255767; PubMed=8197457;
 RA Meyer K., Leube M.P., Grill E.;
 RT "A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis thaliana."
 RL Science 264:1452-1455 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=leaf;
 RX MEDLINE=95007758; PubMed=7923358;
 RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
 RT "The A. thaliana disease resistance gene Rps2 encodes a protein containing a nucleotide-binding site and leucine-rich repeats."
 RL Cell 78:1089-1099 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=leaf;
 RX MEDLINE=94255766; PubMed=7910981;
 RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F., Giraudet J.;
 RT "Arabidopsis ABA response gene AB11: features of a calcium-modulated protein phosphatase."
 RL Science 264:1448-1452 (1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Scheller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Striekema W., Entlian K.-D., Terryn N., Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Weisenseigartner M., de Simone V., Obermayer B., Macho R., Mueller M., Kreiser B., Deleney M., Pilsdomech P., Watson M., Schmidheini T., Reicher B., Portetalle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P., Langham S.-A., McCullagh B., Billham L., Robben J., Van der Schueren J., Grymoprez B., Chuang Y.-D., Vandenbusche F., Braeken M., Weltjens I., Voet M., Baetiaens I., Aert R., Defoor E., Weltzenegger T., Bothe G., Rampeger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirks W., Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koeltter P., Berner S., Hempel S., Feldausch M., Lamberth S., Van den Daele H., De Keyser A., Buyssehaert C., Gielen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Alten K., Clark L., Doggett J., Hall S., Kay M., Lennard N., Mcay K., Mayes R., Petrelet A., Rajandream M.A., Lyne M., Benes V., Reckmann S., Borkova D., Bioecker H., Scharfe M., Grimm M., Loehner T.-H., Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., Gabai C., Fuchs M., Fartmann B., Grandenath K., Dauner E., Herzl A., Neumann S., Argitlou A., Vitale D., Lignori R., Piravandi E.,

RA Massenet O., Quigley F., Clabaud G., Wendlein A., Felder R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., RA Schabador F., Cooke R., Berger C., Montfort A., Casacuberta E., RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A., RA Perez-Perez A., Purrelle B., Bent E., Johnson S., Tacon D., Jesse T., RA Heijnen L., Schwarz S., Scholler P., Heber S., France P., Belke C., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Parnell L., Dedha N., Gnoj L., Schütz K., Huang E., Spiegel L., RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., RA Lacroix P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., RA Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., RA Du H., Ali J., Berghoff A., Jones K., Dione K., Cotton M., Joshi C., RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., RA Swaby I.K., O'Shaughnessy A., Rodriguez W., Hoffman J., Till S., RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A., RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana";
 RL Nature 402:769-777 (1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the RSP consortium (Salk/Stanford/PGRC)."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN ABSICISIC ACID (ABA) SIGNALING PATHWAY.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC
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 CC
 CC EMBL; X78886; CA55484.1; -;
 CC EMBL; U12856; AA50237.1; -;
 CC EMBL; X77116; CA54383.1; -;
 CC EMBL; AL049483; CAB39673.1; -;
 CC EMBL; AL161564; CAB79463.1; -;
 CC EMBL; AY035073; AAK59578.1; -;
 CC HSSP; P35813; 1A60.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR001932; PP2C-like.
 CC InterPro; IPR002221; PP2C.
 CC Pfam; PF00481; PP2C; 1.
 CC SMART; SM00331; PP2C_SIG; 1.
 CC SMART; SM00332; PP2C_C; 1.
 CC PROSITE; PS00018; EF_HAND; 1.
 CC PROSITE; PS10032; PP2C; 1.
 CC KX HydroLase; Magnesium; Manganese; Multigene family; Calcium-binding.
 CC FT CA BIND 93 104 EF-HAND (POTENTIAL).
 CC FT DOAMN 417 420 POLY-VL.
 CC FT VARIANT 180 180 G->D (MUTY PHENOTYPE AND ABA-
 CC FT CONFLICT 24 24 G->R (IN REF. 5).
 CC FT CONFLICT 105 105 I->V (IN REF. 1).
 CC SQ SEQUENCE 434 AA; 47505 MM; 4A4CS4F04195F572 CRC64;
 Alignment Scores:
 Pred. No.: 7.05e-18 Length: 434
 Score: 352.50 Matches: 125
 Percent Similarity: 44.71% Conservative: 65

US-09-935-124A-1 (1-1422) × P2CL_ARATH (1-434)	Best Local Similarity: 29.41%	Mismatches: 148
Query Match: 13.77%	Indels: 87	
DB: 1	Gaps: 19	
105 GACCTCTTGGGGGACCTTCGCGACCCGACCGC--TCGCGCGCCGCGCTGCCGGGAA 161		
45 AspMetMetValSerLeuProGluThrSerCysSerValSerGlySerHisGlySer 64		
162 GAAGCTCAGAAAGAACCCCTGCTCTTGATGACCTCCCTCGCGACGACTACTGACTCA 221		
65 GluSerArgLysValLeuIleIleSerArgLysLeuSerProMetLeuMetLysGluSer 84		
222 GGATCAGGGGGAACCTTCTCTTGTGATGATCTCCACCCGCTAGCACTGCGCAT----- 275		
85 AlaAlaAlaAspIleValValValAsp-----IleSerAlaGlyAspGluIle 100		
276 TCAAGTCTCTTGGCACAATCAATATCCAGATGTA--AAGACTGAAGGAAAGAGCA 332		
101 AsnGlySerAspIleThrSerGluLysMetIleSerArgThrGlu----- 116		
333 AAGAGAAAACTCCGAGAAAGAGAAATGCAAGTGAAGACTTGTCGAAAAAAGTT 392		
117 -----SerValProLeuTyrGlyPheThrSerIleCys-----GlyArg 124		
393 TGTAAAGCCTCTTGCGATCTTGTGATGAGGAGGCTATGTGGCTAGCGGAAGGGTAG 452		
125 -----SerValProLeuTyrGlyPheThrSerIleCys-----GlyArg 137		
453 AAGGAGAGAGATGACGAATGGCCACGATCATCTGAACATCAACGAGAGTGAAGGCC 512		
138 ArgProGluMetGluAspAla-----ValSerThrIleProArgPheLeuGlnSer 154		
513 CAAATGCTCCCTCAAT-----ACTCGGCTTCAATATTTGCT 548		
155 SerSerGlySerMetLeuAspGlyArgPheAspProGlnSerIleAlaHisPhePheGly 174		
549 GTTTTGTATGACATGAGAGAAATTCGAGCTCAAAATTTGCTGCACGAATTTGACTCA 608		
175 ValTyrAspGlyIleGlyIleSerGlnValAlaAsnTyrCysArgGluAspMetHisLeu 194		
609 AACTTAATCAAAAAATTTCTTAA-----GGAGATGTAATCACT 647		
195 AlaLeuAlaGluGlnIleAlaLysGluLysProMetLeuCysAspGlyAspThr---Tyr 213		
648 GTAGAGAAAACCGTAAAGAGATGCGCTTTTGGACACTTTCAGACATTAAGTGAAGAGTTC 707		
214 LeuGluLysTyr---LysLysAlaLeuPheAsnSerPheLeuArgValAspSerGluIle 232		
708 CTTAAACAAGCTTCGAGCCAAAGACCTCGCTGGAAAGATGGGTTCACCTGCACGCTGTGTT 767		
233 GluSerValAlaProGluThrVal-----GlySerThrSerValAla 247		
768 CTGCGCTGTGACAACTTTTATATTTGCAACCTCGAGATAGTGGGCAACTTGTGT 827		
248 ValValPheProSerHisIlePheValAlaAsnGlyAspSerArgAlaValLeuCys 267		
828 CGTTTATATGAGAGAGATCAAAACATGCAAGCTTAAAGCTTACGAGAAAGCAATATCA 887		
268 Arg-----GlyLysThrHisLeuProLeuSerValAspHisLysPro 281		
888 ACTCAAGTAAAGAGACCGGATGAGATCAAGAAAGCTGCAGAAAGCTC-----ACG 938		
282 AspArgGluAspGluAlaAlaArgIleGluAlaAlaGlyLysValIleGlnTyrAsn 301		
939 GATGGCGGTGTTTGGCGCTCTAGAGCTGTCACGCTCATTTGGGAGCGGACAGTACAG 998		
302 GlyAlaArgValPheGlyValLeuAlaMetSerArgSerIleGlyAsp---ArgTyrLeu 320		
999 CGCTGGCGGTCACTCTGTGTGCGGACATCAAGCGCTGCACAGTCAACCCCATATGACAG 1058		
321 LysProSerIleIleProAspProGluValThrAlaValLysArgValLysGluAspArg 340		

QY 1059 TTCATTGTTGGCTGTATGAGCGCTTCAAGGTCCTTAACCCCAAGAAGCCGTAAAC 1118
Db 341 CysLeuIleuAlaSerAspGlyValTrpAspAlaMetThrAspGlutIuaLcYgdu 360

QY 1119 TTCATC-----TTCGC 1130

Db 361 MetAlaAsglyAsnArgIleuLeuEntRphIsLysLysAsnAlaValAlaGlyAspAlaSer 380

QY 1131 TGTCTCGAGATGAAAAAGATCCAGACC CGGAGAACGAATCGCGACCGACGCCCGCTAC 1190

Db 381 LeuAlaAlaAspGlnGlyArgLysSgluIuLys-----AspProAlaLa 395

QY 1191 GAAGCACGCTTGCAACAGCGCTGCACCAAGCGCGTGCAGCGGCGCTCGCCGCAACATGC 1250

Db 396 MetSerAlaAlaGluTrpLeuSerLysLeuAlaIleGlnArgGlySerLysAspAsnIle 415

QY 1251 ACTGATGATGTGTG 1265

Db 416 SerValValValVal 420

RESULT 6
P2C2_CABEL STANDARD; PRT; 356 AA.

ID P2C2_CABEL AC P49596;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein phosphatase 2C T23F11.1 (BC 3.1.3.16) (P2C).
GN T23F11.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Pelodetritinae; Caenorhabditis.
CX NCBI_TaxId=6239;
RN NM_007111.1
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol NZ.
RA Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RL Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RE REVISIONS.
RF Durbin R.;
CC -Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC -CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
CC -1-COPOLYMER: BELONGS TO THE P2C2 FAMILY.
CC -1-SIMILARITY: BELONGS TO MANGANESE IONS (BY SIMILARITY).

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CC or send an email to license@ebi.ac.uk).

CC -----
CC EMBL; Z46343; CAAG6456.2; .
CC HSSP; P35813; 1A60.
DR WormSep; T23F11.1; CEZ4009.
DR InterPro; IPRO001933; P2C2-like.
DR InterPro; IPRO00222; P2C2.
DR Pfam; PF00481; P2C2_1.
DR SMART; SM00332; P2C2_Sig_1.
DR SMART; SM00332; P2C2_1.
DR PROSITE; PS01032; P2C2; 1.
KW Hypothetical protein; Hydrolase; Magnesium; Manganese.
FT METAL 37
FT METAL 37
FT METAL 38
FT METAL 59
FT METAL 228
FT METAL 277
SQ SEQUENCE 356 AA; 39064 MW; ECDB0841CFB026B5 CRC64;

Alignment Scores:

Pred. No.:	1,54e-17	Length:	356
Score:	347.50	Matches:	103
Percent Similarity:	48.63%	Conservative:	57
Best Local Similarity:	31.31%	Mismatches:	108
Query Match:	13.57%	Indels:	61
DB:	1	Gaps:	13

US-09-935-124A-1 (1-1422) x P2C2_CABEL (1-356)

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QY 372 GAGCTTGAGAAAAGAAAGCTTTTAAGCTCTTCGCTGATCTTGGTGAAGGCTAT 431
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DB 3 GlnThrLeuSerLysProValThrLysLysGluSerLysSerCysAlaasnGluAsnTyr 22
QY 432 GTGGCTGAG-----CGGAAGGCTGAGAGGAGAGATGAGATGAGATGCCCATC 482
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 23 LeuValGlySerSerCysMetGlnGlyTPRArgValAspMetGluAspAlaHisThrHis 42
QY 483 CTGAACGACATCACCGAGAGGTGTAGCCCCCATGCTCCCTCATTAAGCTGGTTTCAT 542
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 43 LeuLeuSerLeuProAspAsp-----ProLysCysAlaPhe 54
QY 543 TTTCGCTTTTGAAGAGATGAGAAATTCGACCTCAAAATTCCTGCACAGATTGG 602
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 55 PheAlaValTyrAspGlyHisGlyGlySerLysValSerGlnTyrSerGlyLeuAsnLeu 74
QY 603 CATCAAAACTTATC-----AGAAATTTCCTAAGAGAGATGA---ATCAGTGTAGAG 653
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 75 HisLysLysValValAlaGlnLysGluPheSerGlnGlyAspMetLysGluAlaLeuGlu 94
QY 654 AAAACGGTAAGAGATGCTTTTGAACACTTTCAGCATACTGATGAGAGATTCCTTAAA 713
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 95 LysGlyPheLeuGlu-----LeuAspGlnGlnMetArgValAspGluThrLysAsp 112
QY 714 CAAGCTTCCAGCCAGAGAGCTGCTGAAAAGATGGCTCCACTGCCACGCTGTTCTGCT 773
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 113 AspValSer-----GlyThrThrAlaValAlaValLeuLeu 124
QY 774 GTAGACAACTTATTTATATTCGCAACTCGAGATAGTCGGCAATCTTGTCGTTAT 833
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 125 LysGluGlyAspValTyrCysGlyAsnAlaGlyAspSerThrGlyAlaValSerValVal 144
QY 834 AATGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAAAGATCAATCAACTCAG 893
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 145 GlyGlu-----AlaArgProLeuSerPheAspHisLysProSerHis 158
QY 894 TATGAAGACGATGATGATACAGAAAGCTGAGAGAAAGTCAAGGATGGCTGTTTG 953
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 159 GluThrGluAlaArgArgIleIleAlaAlaGlyTyrValGluPheAsnArgValAsn 178
QY 954 GCGCTGCTAGAGGTGTCAGCTTCATTTGGGACGGGACATCAAAAGCTGCGGT----- 1007
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 179 GlyAsnLeuAlaLeuSerThrAlaLeuGlyAspPheAlaPheLysAsnGlyAspThrLys 198
QY 1008 -----GTCACTCTGTGCCGACATGACAGCGCTGACAGCTGACGATCCCC 1049
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 199 ProAlaGluGluGlnIleValThrAlaPheProAspValIleThrAspLysLeuThrPro 218
QY 1050 AATGACAGCTCATTTTGTGGCTGTGATGGCTTTCAAGCTTTTACCCACAGAA 1109
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 219 AspHisGluPheIleValLeuAlaCysAspGlyIleTyrAspValMetThrAsnGlnGlu 238
QY 1110 GCGGTGAATCTGATCTTGTCTGTCTCGAGATGAAAGATCCAGACCGGGAGAGGAAG 1169
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 239 ValValAspPheVal-----ArgLys--Lys 246
QY 1170 TCCGAGACGAGCCCGCTACAGAGAGCTGCAACAGCTGGCCAAAGCGCGTG--- 1226
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 247 LeuAlaGluLysArgAspProGlnSerIleCysGluGluLeuLeuThrArgCysLeuAla 266
QY 1227 -----CAGCGGGGCG-----TCGCGCCACACAGCTCATCTGTGATGGTGGCGATA 1271
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 267 ProAspCysGlnMetGlyGlyLeuGlyCysAspAsnMetThrValValLeuVal----- 284

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QY 1272 GGGCACTGAGGGTGGCGCGCGCCAG 1298
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DB 285 -----GlyLeuLeuHisGlyGln 290

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RESULT 7

ID	P2CA_BOVIN	STANDARD;	PRT;	382 AA.
AC	062829;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (P2C- α).			
GN	PPM1A.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Retina;			
RX	MEDLINE=98146173; PubMed=9486768;			
RA	Klump, S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;			
RT	"Protein phosphatase type-2C isozymes present in vertebrate retinae:			
RT	purification, characterization, and localization in photoreceptors."			
RL	J. Neurosci. Res. 51:328-338(1998).			
CC	- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.			
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +			
CC	phosphate.			
CC	- COPFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.			
CC	- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE P2C FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isdb-sib.ch/announce/			
CC	or send an email to license@isdb-sib.ch).			
CC	-----			
DR	HSSP; AJ005457; CAA0554.1; -.			
DR	HSSP; P35813; 1A6Q.			
DR	InterPro; IPR001932; P2C-like.			
DR	InterPro; IPR000222; P2C.			
DR	Pfam; PF00481; P2C; 1.			
DR	SMART; SM00331; P2C-SIG; 1.			
DR	SMART; SM00332; P2C; 1.			
DR	PROSITE; PS01032; P2C; 1.			
KW	Hydrolase; Magnesium; Manganese; Multigene family.			
FT	METAL 37 38	MANGANESE 1 (BY SIMILARITY).		
FT	METAL 38 38	MANGANESE 1 AND 2 (BY SIMILARITY).		
FT	METAL 60 60	MANGANESE 1 (BY SIMILARITY).		
FT	METAL 239 239	MANGANESE 2 (BY SIMILARITY).		
FT	METAL 282 282	MANGANESE 2 (BY SIMILARITY).		
SQ	SEQUENCE 382 AA; 42529 MW; A716B3FA0B7821C2 CRC64;			

Alignment Scores:

Pred. No.:	3.9e-17	Length:	382
Score:	342.00	Matches:	101
Percent Similarity:	49.33%	Conservative:	47
Best Local Similarity:	33.67%	Mismatches:	104
Query Match:	13.36%	Indels:	48
DB:	1	Gaps:	12

US-09-935-124A-1 (1-1422) x P2CA_BOVIN (1-382)

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QY 417 GGTGGAAGGGGTATNGTGTGAGCGGAAGGTGAGAGAGATGACAGATGCCAC 476
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DB 21 GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTPRArgValGluMetGluAspAlaHis 40
QY 477 GTCATCTGAACGACATCACGAGAGGTGTAGGCCCATGCTCCCTCATTAAGTGGGTT 536

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Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---Tyr 53
QY 537 TCATATTTTGTCTTTTGTATGATGACATGAGAAATTCAGACCTCAAAATTTGTGTGCACAG 596
Db 54 SerPhePheAlaValIleYAspGlyIleAlaGlySerGlnValAlaIleYAspGlyIle 73
QY 597 AATTGTCATCAAACTTATTCAGAAATTTCCCT---AAAGAGAT-----GTATACAGT 647
Db 74 HisLeuLeuAspHisIleIleThrAsnAsnGlnAspPheIleGlySerAlaGlyAlaProSer 93
QY 648 GTAGAGAAAACCGTAGAGAGATGCGCTTTTGTGACATTTCAACATCATGTATGAAGAGTTTC 707
Db 94 ValGlu---AsnValIleAsnGlyIleArgThrGlyPheLeuGluIleAspGlnHisMet 112
QY 708 CTTAAACAGCTTCCAGACGACCTGGAAGATGGGTCCATGGGTCCAGCTGAGTGTGTT 767
Db 113 ArgValMetSerGluIleYAsnGlyIleAlaAspArgSerGlySerThrAlaValAlaGlyVal 132
QY 768 CTGGCTGTAGACAAATCTTATATGATGATCCAGCTGCGAGATAGTGGGCAATCTTGTT 827
Db 133 LeuIleSerProGlnHisIleThrIlePheIleAsnGlyIleAspSerAlaGlyIleLeuLeuCys 152
QY 828 CATTATATGAGAGAGATCAAAAACATGACGCTTAAAGCTTCAGCAAAAGACATTAATCCA 887
Db 153 Arg-----AsnArgIleValIleYAspPheThrGlnAspHisIleYAspPro 166
QY 888 ACTCACTATGAAAGACGGATGATGAGATACAGAAAGCTGAGAAACGTACAGGATGGAGCTT 947
Db 167 SerAsnProLeuGlnIleYAsnGlyIleGlnAsnAlaGlyIleYAspValMetIleGlnArg 186
QY 948 GTTTTGGGCTGCTAGAGAGTGTCAAGCTCCATTTGGGAGCGGACAGTACAGACGCTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlnIleAspPheArgIleYAspVal 205
QY 1005 -----GGTGTCAAC-----TCTGTCCCGCAGCATCAGA 1031
Db 206 HisGlyIleYAsnGlyProThrGlnGlnIleValSerProGlnProGlnValHisAspIleGln 225
QY 1032 CGGTCCGACGTGACCCCAATGATGAGATGATTTGTGTGGCTGTGATGGGCTTTTCAG 1091
Db 226 ArgSerGlu-----GluAspArgGlnPheIleIleLeuAlaCysAspArgIleIleTyrParg 243
QY 1092 GTCTTTACCCCAAGAAAGACCGGTGATCTTCTGCTGTCTGAG-----GATGAA 1145
Db 244 ValMetGlyIleAsnGlnIleYAsnGlyIleValIleArgSerArgLeuGlnValIleHisAsp 263
QY 1146 AAGATCCAGACCCGGGAAAGGAAAGTCCGACGCCGCTTACGAAGACGCTTGCAAC 1205
Db 264 -----LeuGlnIleYAsnValIleValIleValIleValIleValIleValIleValIle 269
QY 1206 AGGCTGAGCCCAAGACGCGGTGACGCGGCTCGGCGGACAGCATGATGATGATGCTG 1265
Db 270 GluValIleValIleAspThrCysLeuIleYAsnGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 8
FEM2_RAT STANDARD; PRT; 450 AA.
AC Q9WVR7;
DT 15-JUN-2002 (rel. 41, Created)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
DE (Cam-kinase phosphatase) (CamKase).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99279559; PubMed=10348902;
RA Kitani T., Ishida A., Okuno S., Takeuchi M., Kameehita I.,

RA Fujisawa H.;
RT "Molecular Cloning of Ca2+/Calmodulin-dependent protein kinase
RL J. Biochem. 125:1022-1028(1999).
CC -1- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
CC kinase II activated upon autophosphorylation, and Cam-kinases IV
CC and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: Associates with FlapA (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AB023634; BA82477.1; -.
CC InterPro: IPR000222; PP2C.
CC InterPro: IPR001932; PP2C-like.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00332; PP2Cc; 1.
CC SMART; SM00331; PP2C-STG; 1.
CC PROSITE; PS01032; PP2C; 1.
CC HYDROLASE; Magnesium; Manganese; Apoptosis; Multigene family.
CC DOMAIN 99 109 POLY-GLU.
CC METAL 356 356 MANGANESE 2 (BY SIMILARITY).
CC METAL 400 400 MANGANESE 2 (BY SIMILARITY).
CC SEQUENCE 450 AA; 49165 MW; 67626542F32B2P50 CRC64;

Alignment Scores:
Pred. No.: 4,41e-17 Length: 450
Score: 341.50 Matches: 124
Percent Similarity: 44.31% Conservative: 63
Best Local Similarity: 29.38% Mismatches: 160
Query Match: 13.34% Indels: 75
DB: 1 Gaps: 16

US-09-935-124A-1 (1-1422) x FEM2_RAT (1-450)
QY 108 CTCCTTGGGAGACCTGCGCGAGCCGAGCGCTCGCGCGCTGCCGGAAGAAAGCT 167
Db 25 LeuLeuGlnAspPheProAlaProLeuSerLeuGlnSerProLeuProTyrPys----- 42
QY 168 CAGAAAGACCCCTGCTCTTTGATGATCTCCCTCGGCGACGATGATGATCA 227
Db 43 ValProGlyIleValIleLeuIleGlnIleValIleGlnIleValIleLeuIleValMet 62
QY 228 GGGGACCTTTGCTTTTGTATGATCTCCACCCGCTGACGATGCGATTCAGGTTCTCTT 287
Db 63 GlyPhe---LeuIleYAsnArgSerGlnAsnAlaProProAlaValAlaIle---AlaIleValIleThr 79
QY 288 GCCACATCATATATCCAGATGTTAAAGACTGAAGAGGAAAGAGCAAAAGAAACCTTCC 347
Db 80 HisGlnAlaIleSerGlnIleLeuIleGlnIleThrAspSerGlnIleYAsnProGlu 99
QY 348 GAGGAGAGAGAGAGATGCGCTGAAGAG-----CTTGTGAGAAAGAAA 389
Db 100 GlnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 119
QY 390 -----GTTGTAAACCTCTTCGCTGATC 413
Db 120 GlyLeuSerArgSerPhePheAsnGlyIleProGluValIleYAsnSerGlnIleGlnIleYAsn 139
QY 414 TTTGCTGTGAAGGCTATATGCTACGCGAG----- 446
Db 140 ValProLeuThrIleGlnIleAlaProGlnIleYAsnIleValSerIleHisAlaIleArg 159

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Oy	447	GGTGAGGGAGGAGGACAGAGATGCCCATCTGCATCGTAACAAGCATCCAGAGAGTGT	506
Db	160	AenThraDgaDgLyvMeGeLueArghIvaLSerLue-----	172
Oy	507	AGGCCCCCAGTCGTCCTCAATTACTCGGGTTCA-----	TATTTTGCT 548
Db	173	--ProAlaPheAnHLeuPheGLyLeuSerAarSerValHiIsArgLaIatyrPheLa	191
Oy	549	GTTTTTGATGGAACATGAGAAGAAATTCGAGGCTCCAAAATTGCTGCACAGAATTGCTACA	608
Db	192	VaLPheArGrLyHnIGLyGLyVaLaSRPaLaLaARgyrLaSeArValHiISvalHiStrHr	211
Oy	609	AACTTAATCACAGAAATTTCTTAAGAGAGATGTATACAGTGTATAAGAAAAACCGTAAGAGA	668
Db	212	AenAlaSerHnIGln--ProGlu-----	LeuethrAsrProAlaLa 225
Oy	669	TGCTTTTGGACACTTTTCAMAGCATCTGATGAAGAAGTTCTTAAACAGCTTCCAGCCAG	728
Db	226	ALaleuLySvGIuaLPheArGHnleThrAsrGLmeArcheuIndInLyLaIayArGrLI	245
Oy	729	AAAGCTGCTGGAAAAGATGGTGCACCTGCCACGCTGGTGTGCTGTGTGTATAACAATCTT	788
Db	246	Arg-----LeuGlnSerGrLyTHrThGlYvaLCysAlaLeuILeHxGLyaLaLeu	263
Oy	789	TATATTTCCAACSTCCGAGATAGCGGGCAATCGTGTGTTATTAATAGAGAGATCAA	848
Db	264	HiEvAlaIatPrLeGLyHarSerGlnValIIleuEuaI-----	Gln 277
Oy	849	AAACATGACGCTTAAAGCTCCAGCAAGAACATATATCCAACTAGTATGAAGAGCGAGTG	908
Db	278	GlnGLyGlnValValLyVleuMerGlnProHISlyVerGroLyuArGLInArGrLIuLySer	297
Oy	909	AGGATACAGAAAGCTGGAGAAAGCTGACG-----	GATGGCGGTGTTTGAGCGCTG 959
Db	298	ArgIIleGlnLaLeuGlyGLyPheValISerLeuMerAAsrCystrGrArValanGLyThr	317
Oy	960	CTAGAGGCTGACAGCTCATGTCGGGGAAGGGACAGAACAGGCGGCTGGCTGTGG	1019
Db	318	LeuAlaValISerAaGLaIIleGlyArP---ValPheGlnLyVerGroLyValSerGLyLu	336
Oy	1020	CCCGACATCAGACGCTGCGAGCTGACSCCCCAATGACAGGTTCAITTTGTGGCTGTGAT	1079
Db	337	AlaArerAlaIaSerArGrLyLeuHthrGLyLeuGlnArGrLyLeuHeuLeuLaCyArP	356
Oy	1080	GGGCTCTTCAGAGCTTTTACCCCAAGAAAGCCGTGAATCTCATCTTGTGCTGTGCAG	1139
Db	357	GlyPhePheArVerValIaProHnIHnIGLnILeProGLyLeuValHIISglYnIleuLeu	376
Oy	1140	GATGAAAGATCCAGACCCCGGAAAGGGAATCCGCGAGCCGAGCCGCGCTACGAAAGCACC	1199
Db	377	ArgGlnLyv-----GlySerGLyMerChIVaLaIISgluI-----	387
Oy	1200	TGCAACAGGCTGGCCCAACAGGCGSGTTCAGAGCGGGCTGGCGGACAACTCATCTGTGAT	1259
Db	388	-----GluLeuValLaIaValaLaIaArGrAaRgGLySerHnIAArPnHleThrValMet	405
Oy	1260	GTGTGTG 1265	
Db	406	ValVal 407	
RESULT 9			
P2CA_RABIT		STANDARD;	PRT; 382 AA.
ID_P2CA_RABIT			
AC_P35814			
DT_01-JUN-1994	(Rel. 29, Created)		
DT_01-JUN-1994	(Rel. 29, Last sequence update)		
DT_16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Protein phosphatase 2C alpha Iboform (EC 3.1.3.16) (PP2C-alpha) (IA)		
GN	PPM1A OR PPM1A.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		

OX	NCHI_TaxID=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
XC	MEDLINE=92182001; PubMed=1311954;
RA	Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT	"Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RL	comparative analysis of amino acid sequences.";
CC	Biochim. Biophys. Acta 1130:100-104(1992).
CC	- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
CC	- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC	- SUBUNIT: MONOMER.
CC	- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC	-----
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CC	tion between the Swiss Institute of Bioinformatics and the EMBL outstat-
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CC	entities requires a license agreement (See http://www.isb-sib.ch/anno
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; S8757; AAB21783.1; -.
DR	PIR; S22422; S22422.
DR	HSSP; P35813; IA6Q.
DR	InterPro; IPRO01932; PP2C-1like.
DR	InterPro; IPRO00222; PP2C.
DR	Pfam; PF00481; PP2C_1.
DR	SMART; SM00331; PP2C_STG; 1.
DR	SMART; SM00332; PP2C; 1.
DR	PROSITE; PS01032; PP2C; 1.
KW	Hydrolase; Magnesium; Manganese; Multigene family.
FT	METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT	METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT	METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT	METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT	METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ	SEQUENCE 382 AA; 42462 MW; 46BCF1854FD1CA86 CRC64;
Alignment Scores:	
Pred. No.:	5,44e-17 length: 382
Score:	340.00 Matches: 101
Percent Similarity:	49.33% Conservative: 47
Best Local Similarity:	33.67% Mismatches: 104
Query Match:	13.28% Indels: 48
DB:	Gaps: 12
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OY	417 GATCTGAAGGGCTATTGTGGCTGACCGGAGGGTGAGGAGGAGATGCAGATGCCAC 476
Ddb	: : : : : :
Ddb	21 GtlyenAangryrGtlyleusenSerMetclndcIyTrparyGalwetGtlwBralahIs 40
OY	477 GTCATCTGAAACAATCACATACCAGGAGAAGTAGAGCCCCCATCGTCCTCATTAATCGGGTT 536
Ddb	::: :::: : : : : :
Ddb	41 ThrAlaValIIegIyleu-----ProsergIyeugInthr---Trp 53
OY	537 TCATATTGTGTTTTGTATGACATGAGGAATTCGAGCCCAAATTTGGTCGACAG 596
Ddb	: : : : : :
Ddb	54 SerPhePreAlaValIyrArpeglYhlalagIsetlnvalAlalystryCyvSwglu 73
OY	597 AATTTCATCAAAACTTATATCAGAAAATTTCCT---AAAGAGAT-----GTAAATCAGT 647
Ddb	::: : : : : : : : : : : :
Ddb	74 HisIeuIeuAephstIetlrHnAenGlnaAepheylselYerAlaGlyAlaProser 93
OY	648 GTAAGAAAAACGTGAAGAGATGCTTTTGACACTTTCAAGATACTGATGAAGAGTTT 707
Ddb	: : : : : :
Ddb	94 ValGlu--AenValIysAsnglYllleArgThrGlyPheIeuGIurIleaergIHmeC 112
OY	708 CTTAAACAAGCTTCCACGACGAGACCTGCTGCGTGAAGAAAGATGGTTCACATGCGACGTGT 767
Ddb	::: :::: : : : : :

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Db 113 ArgValMetSerGluValSerHisGlyAlaAspArgSerGlySerThrAlaGlyVal 132
Qy 768 CTGGCTGTAGACAACTTTTATTATTCGACCTCGAGATAGTGGGCAATTTGTGT 827
Db 133 LeuIleSerProGlnHisThrTyPheIleAsnCyGlyAspSerArgGlyLeuLeuCyS 152
Qy 828 CGTTATATATAGAGAGATCAAAAACATGCAGCCTTAAGCTTCAGCAAAAGCATATCCA 887
Db 153 Arg-----AsnArgLysValHisPhePheThrGlnAspHisLysPPro 166
Qy 888 ACTCACTATGAAAGCGGATGAGATACAGAAAGCTGAGAAAGCTGACGAGATGGCGT 947
Db 167 SerAsnProLeuGlnLysGlnArgIleGlnAsnAlaGlyLysSerValMetIleGlnArg 186
Qy 948 GTTTGGGCGCTGTAGAGTGTCAAGCTCCATTCGGGAGCGGCGCATCAAGCGCTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
Qy 1005 -----GGTGTACC-----TCGTGCCCGCATCATCA 1031
Db 206 HisGlyLysGlyProThrGlnGlnLeuValSerProGlnProGlnValHisAspIleGln 225
Qy 1032 CGGTGCGACCTGACCCCAAGACAGAGTGTGATTTTGTGGCTGTGATGGGCTTTCAG 1091
Db 226 ArgSerGlu-----GlnAspAspGlnPheIleIleLeuAlaCyAspGlyTyrLeuPasp 243
Qy 1092 GTCTTTATCCCAAGAAAGCGGTGACCTTCACTTCTCTCTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnGlnLeuCyAspPheValArgSerArgLeuGlnValThrAspAsp 263
Qy 1146 AAGATCCAGACCCGGGAAAGGAAAGTCCGACCGACGCGCGGTACGAAAGAGCCTGCAC 1205
Db 264 -----LeuGlnLysValCyAsn 269
Qy 1206 AGCTGCGCAACAGACGCGGTGACGCGGCTCGGCGCAACGTCATCTGATGGTGTG 1265
Db 270 GluValValAspThrCysLeuTyrGlySerArgAspAspMetSerValIleLeuIle 289
RESULT 10
P2CA RAT STANDARD; PRT; 382 AA.
ID P2CA RAT
AC P20650;
DT 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Protein phosphatase 2C, alpha isoform (EC 3.1.3.16) (P2C-alpha) (IA)
GN (Protein phosphatase 1A).
GN PPM1A OR PPM1A OR P2C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=89184515; PubMed=2538815;
RA Tamura S., Lynch K.R., Larner J., Fox J., Yasui A., Kikuchi K.,
RA Suzuki Y., Tsukui S.;
RT "Molecular cloning of rat type 2C (1A) protein phosphatase mRNA.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch.
CC -----
Cc EMBL; J04503; AAA1917.1; -.
Dr PIR; A32399; A32399.
Dr HSSP; P35813; 1A60.
Dr InterPro; IPR001932; P2C-like.
Dr InterPro; IPR000222; P2C.
Dr Pfam; PF00481; P2C; 1.
Dr SMART; SM00331; P2C_Sig; 1.
Dr SMART; SM00332; P2CC; 1.
Dr PROSITE; PS01032; P2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family.
FT METAL 37 37
FT METAL 38 38
FT METAL 60 60
FT METAL 239 239
FT METAL 282 282
SQ SEQUENCE 382 AA; 42416 MW; C1C386B935374F89 CRC64;
Alignment Scores:
Pred. No.: 5,44e-17 Length: 382
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 46
DB: Gaps: 12
US-09-935-124A-1 (1-1422) x P2CA_RAT (1-382)
Qy 417 GGTCTGAAGGCTATGTGTGCTAGCGGAGGCTGAGAGGAGAGATGCAGATCCAC 476
Db 21 GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyrArgValIleuLeuAspAlaHis 40
Qy 477 GTCAATCTTCAACGACATCAACCGAGAGGTAGAGCCCATCGTCCCTCATTAATGGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGlnThr---Trp 53
Qy 537 TCATATTTTCTGTATTTTATGATGACATGAGAAATTCGACCTCAAAATTTCTGCACAG 596
Db 54 SerPhePheAlaValTyrAspGlyHisAlaGlySerGlnValAlaLysTyrCysGly 73
Qy 597 AATTGGATCAAAAATTATTCAGAAAATTTCT---AAAGGAAAT-----GTATTCAGT 647
Db 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLysGlySerAlaGlyAlaProSer 93
Qy 648 GTAGAGAAAACCGTGAAGAGATGCTTTTGGACACTTTCAGACTACTATGAAGATTC 707
Db 94 ValGlu---AsnValLysAsnGlyLysLeuArgThrGlyPheLeuGlnLysAspGlnHis 112
Qy 708 CTTAAACAGCTTCACGCCAGCAAGGCTGCGAAAGATGGCTCCACTGCCAGTGTGT 767
Db 113 ArgValMetSerGluLysHisGlyAlaAspArgSerGlySerThrAlaGlyVal 132
Qy 768 CTGGCTGTAGACAACTTTTATTATTCGACCTCGAGATAGTGGGCAATTTGTGT 827
Db 133 LeuIleSerProGlnHisThrTyPheIleAsnCyGlyAspSerArgGlyLeuLeuCyS 152
Qy 828 CGTTATATATAGAGAGATCAAAAACATGCAGCCTTAAGCTTCAGCAAAAGCATATCCA 887
Db 153 Arg-----AsnArgLysValHisPhePheThrGlnAspHisLysPPro 166
Qy 888 ACTCACTATGAAAGCGGATGAGATACAGAAAGCTGAGAAAGCTGACGAGATGGCGT 947
Db 167 SerAsnProLeuGlnLysGlnArgIleGlnAsnAlaGlyLysSerValMetIleGlnArg 186
Qy 948 GTTTGGGCGCTGTAGAGTGTCAAGCTCCATTCGGGAGCGGCGCATCAAGCGCTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
Qy 1005 -----GGTGTACC-----TCGTGCCCGCATCATCA 1031
Db 206 HisGlyLysGlyProThrGlnGlnLeuValSerProGlnProGlnValHisAspIleGln 225
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Alignment Scores: 7.58e-17 Length: 382

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OY 1092 GTCTTTACCCCAAGAAGACCCTGGAATCTCATCTTGCTCTGTCGAG-----GATGAA 1145  
Db 244 ValMetGlYAmnGlucIuLeucyAspPheValAArgSerArXgluclvalThrSapAp 263  
OY 1146 AAGATTCAGAACCCGGGAGGGAAGTCGCCGACGCCCGCTACGAGACACTTGCAC 1205  
Db 264 -----LeuGluysValCyaaN 269  
OY 1206 AGCGTGGCCCAACAAGCCGCTGACGGGGCTCGGCCGCAACGATCATGTGNGTGcng 1265  
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ID P2CA_MOUSE  
AC P49443;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
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DE (Protein phosphatase 1A).  
GN PPM1A OR PPM1A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RC MEDLINE=94333828; PubMed=8056349;  
RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,  
RA Kanamaru R., Tamura S.;  
RT "The cDNA sequence encoding mouse Mg2+-dependent protein phosphatase  
RL Gene 145:311-312(1994)".  
CC -1 FUNCTION: ENZYME WITH A BROAD SPECIFICITY.  
CC -1 CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
CC phosphate.  
CC -1 COPFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.  
CC -1 SUBUNIT: MONOMER.  
CC -1 SIMILARITY: BELONGS TO THE PP2C FAMILY.  
-----  
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CC EMBL; D28117; BA05662.1; -.  
DR HSSP; P35813; IAQ.  
DR MGD; MGI:99878; Pma.  
DR InterPro; IPRO01932; PP2C-like.  
DR InterPro; IPRO00222; PP2C.  
DR Pfam; PF00481; PP2C; 1.  
DR SMART; SM00331; PP2C_SIG; 1.  
DR SMART; SM00332; PP2CG; 1.  
DR PROSITE; PS01032; PP2C; 1.  
KW Hydroxylase; Magnesium; Manganese; Multigene family.  
FT METAL 37  
FT METAL 38  
FT METAL 60  
FT METAL 239  
FT METAL 282  
SEQUENCE 382 AA; 42432 MW; DC006610E1583870 CRC64;
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Score:	338.00	Matches:	99
Percent Similarity:	48.67%	Conservative:	47
Best Local Similarity:	33.00%	Mismatch:	106
Query Match:	13.20%	Indels:	48
DB:	1	Gaps:	11
US-09-935-124A-1 (1-1422) x P2CA_MOUSE (1-382)			
QY 417	GGTCTGAAGGGCTATGTGGCTGAGCCGAAAGGTGAGAGGAGATGCAGATGCCAC	476	
DB 21	GlyleuArgTyrGlyLeuSerSerMetGlnGlyTTrpArgValGluMetGluAspLeuHis	40	
QY 477	GTCATCCGAAACGACATCACCGAGAGGTGAGGCCCCCATGCTCCCTATTAATCGGGTT	536	
DB 41	ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr--Trp	53	
QY 537	TCATATTTTGGCTGTTTGTATGAGCATGAGAAATTCAGCCTCAAAATTTGCTGCACAG	596	
DB 54	SerPhePheAlaValIlyrAspGlyHisAlaGlySerGlnValAlaIlyrTyrcysGlu	73	
QY 597	AATTTCATCAAACTTAAATCAGAAAATTTCTT-----AAAGAGATGTAATCAGT	647	
DB 74	HisIleuLeuAspHisIleThrAsnAsnGlnAspPheArgGlySerAlaGlyAlaProSer	93	
QY 648	GTAAGAGAAACCGTGAAGAGATGCTTTTGGACATCTTACACATACATGATGAAGATTC	707	
DB 94	ValGlu---AsnValIlyAsnGlyIleArgTyrGlyPheLeuGluIleAspGluHisMet	112	
QY 708	CTTAAACAGCTTCACGCGCAAGACCGCTGGAAGATGGGTTCACGCTCCACGCTGTT	767	
DB 113	ArgValMetSerGluIlyAspHisGlyAlaAspArgSerGlySerThrAlaValGlyVal	132	
QY 768	CTGGCTGTGAGCAACATCTTTATATATGCGCACTTCGAGATAGTCGGGCAATCTTGTT	827	
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QY 828	CGTTATATATGAGAGAGCTCAAAAACATGCAGCCTTAAGCCTCAAGAAAGCATATATCA	887	
DB 153	Arg-----AsnArgIlyValHisPhePheThrGluAspHisIlyAspPro	166	
QY 888	ACTCATGATGAGAGCGGATGAGATGATACAGAAAGGCTGAGAAACGTCAGGGATGGGCT	947	
DB 167	SerAsnProLeuGlnIlyAspGluArgIleGlnAsnAlaGlyIlySerValMetIleGlnArg	186	
QY 948	GTTTGGCGCTGAGAGGTGTGCACGCTCATTTGGGAGAGGGCAGTACAGCGCTGC---	1004	
DB 187	ValAsnGlySerLeuAlaValSerArgAlaLeuGlyIlyAspPheAspTyrIlyS---CysVal	205	
QY 1005	-----GGTGTACC-----TTGTGCGCCGACATTCGA	1031	
DB 206	HisGlyIlyAspGlyProThrGlnGlnLeuValSerProGluProGluValHisAspIleGlu	225	
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QY 1092	GTCCTTATCCCAAGAGAGCGCTGACATTCATCTTGCTCTCGAG-----GATGAA	1145	
DB 244	ValMetGlyAsnGlnGluIlyLeuGlyAspPheValArgSerArgLeuGlnValThrAspAsp	263	
QY 1146	AAGATCCAGACCCGGGAGGGAGAGTCCGACGCCCGCTACGAAAGACGCTGCAC	1205	
DB 264	-----LeuGluIlyValCysAsn	269	
QY 1206	AGGCTGGCCAAAGCGGTGTCAGCCGGGCTGGCGGAAAGTCACTGTATGTTGGTG	1265	
DB 270	GluValIlyAspThrCysLeuTyrIlyGlySerArgAspAsnMetSerValIleLeuIle	289	
RESULT 12			
P2CA_HUMAN			
ID_P2CA_HUMAN	STANDARD;	PRT;	382 AA.
AC	P35813; 075551;		
DT	01-JUN-1994 (Rel. 29, Created)		

DT 01-JUN-1994 (Rel. 29, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE (Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
 GN PPM1A OR PPM1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
 RX MEDLINE=92182001; PubMed=1311954;
 RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
 RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
 RT comparative analysis of amino acid sequences";
 RL Biochim. Biophys. Acta 1130:100-104 (1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
 RX MEDLINE=98372738; PubMed=9707433;
 RA Takekawa M., Maeda T., Saito H.;
 RT "Protein phosphatase 2Calpha inhibits the human stress-responsive p38
 RT and JNK MAPK pathways";
 RL EMBO J. 17:4744-4752 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
 RC TISSUE=Colon;
 RA Strausberg R.;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=97157470; PubMed=9003755;
 RA Das A.K., Helps N.R., Cohen P.T.W., Barford D.;
 RT "Crystal structure of the protein serine/threonine phosphatase 2C at
 RT 2.0-A resolution";
 RL EMBO J. 15:6798-6809 (1996).
 CC -1- FUNCTION: Enzyme with a broad specificity.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -1- SUBUNIT: MONOMER.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
 CC 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 DR EMBL; S87759; AAB21784.1; -;
 DR EMBL; AF070670; AAC28354.1; -;
 DR EMBL; BC026691; AA26691.1; -;
 DR PIR; S22423; S22423.
 DR Genew; HGNC:9275; PPM1A.
 DR MIM; 606108; -;
 DR PDB; 1A6Q; 27-MAY-98.
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR000222; PP2C.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_Sig; 1.
 DR SMART; SM00332; PP2CG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Manganese; Multigene family;
 KW Alternative splicing; 3D-structure.
 FT METAL 37
 FT METAL 38
 FT METAL 60
 FT METAL 239
 FT METAL 282
 FT METAL 324
 VARSPLIC 318 324
 EITKQK -> GGSFNKK (IN ISOFORM ALPHA-2).

FT VARSPLIC 325 382 MISSING (IN ISOFORM ALPHA-2).
 SQ SEQUENCE 382 AA; 42447 MW; D48F508BA476687 CRC64;
 Alignment Scores:
 Pred. No.: 1,06e-16 Length: 382
 Score: 336.00 Matches: 100
 Percent Similarity: 49.00% Conservative: 47
 Best Local Similarity: 33.33% Mismatches: 105
 Query Match: 13.12% Gaps: 48
 DB: 1 Gaps: 12
 US-09-935-124a-1 (1-1422) x P2CA_HUMAN (1-382)
 QY 417 GGTTCGAGGCGCTGATGCTGAGCGGAGCTGACAGAGATGACAGATGATCCAC 476
 DB 21 GYLDUATGTYGLYUENSSERMETGLNLYTPRTGVALGLUWETGLUASPGLAHS 40
 QY 477 GTCACTCTGAAGACATCCAGAGAGGTGAGGCCCATTCGCTCATTACTGGGATT 536
 DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu--Glusertp 53
 QY 537 TCATATTTTGGCTGTTTGTATGACATGAGAGATTGAGCCTCAAAATTTGTCACAG 596
 DB 54 SerPhePheAlaValTyRAspGlyHleAlaGlySerGlnValAlaTyTyCyAcGly 73
 QY 597 AATTGCAATCAAACTTAATCAAGAAATTTCT--AAAGAGAT-----GTATCATG 647
 DB 74 HleuLeuAspHleAlaIleThrAsnAsnGlnAspPheTyGlySerAlaGlyAlaProSer 93
 QY 648 GTAGAGAAACCGTGAAGAGATGCTTTTGAGACATTCATCAATGATGAGAGATTC 707
 DB 94 ValGlu--AsnValTyLeuAsnGlyIleAlaGlyThrGlyPheLeuGlnIleAspGlnHleMet 112
 QY 708 CTTAAACAGGCTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 767
 DB 113 ArgValMetSerGlnTyLeuHleGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
 QY 768 CTGCTGTGACACAACTTTATATGCGCACTGAGATGTCGCGCAATCTGCT 827
 DB 133 LeuLeuSerProGlnHleThrTyPheAlaHleAsnCyGlyAspSerArgGlyLeuLeuCyAs 152
 QY 828 CGTTATATGAG 887
 DB 153 Arg-----AsnArgValValHlePhePheThrGlnAspHleTyLeuPro 166
 QY 888 ACTGATGATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 947
 DB 167 SerAsnProLeuGlnGlnTyLeuGlnAlaGlnHleGlnAlaGlnHleGlnAlaGlnHle 186
 QY 948 GTTTTGCGCTGCTGATGAGGTGTCAAGCTTCATTGGGAGAGCGGAGATGACAGCGTGC 1004
 DB 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlnAlaAspPheAspTyTyLe--CyAsnAl 205
 QY 1005 -----GTTGTCACC-----TCGTGCTCCGACATGACA 1031
 DB 206 HleGlyTyGlyProThrGlnGlnLeuValSerProGlnProGlnValHleAspIleGlu 1225
 QY 1032 CGGTGCGAGCGTACCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1091
 DB 226 ArgSerGln-----GluAspArgGlnPheIleAlaLeuAlaCyAspGlyIleIleTyrAsp 243
 QY 1092 GTCTTATCCCAAG 1145
 DB 244 ValMetGlyAsnGlnGlnLeuCyAspPheValArgSerArgGlnGlnValAlaThrAsp 263
 QY 1146 AAGATTCAGACCCGAG 1205
 DB 264 -----LeuGlnTyValCyAsn 269
 QY 1206 AGGCTGCGCAACAAGCGGCTGACGCGGCTGCGCGGACATGATGATGATGATGATGAT 1265
 DB 270 GluValValAspThrCyLeuTyTyGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 13
 P2C2_ARATH STANDARD; PRT; 423 AA.
 ID P2C2_ARATH
 AC 004719;
 DT 15-DEC-1998 (rel. 37, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last sequence update)
 DE 15-UN-2002 (rel. 41, Last annotation update)
 DE Protein phosphatase 2C AB12 (EC 3.1.3.16) (P2C) (abscisic acid-insensitive 2).
 GN AB12 OR ATG57050 OR MHM17.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta, and cv. Columbia;
 RX MEDLINE=97308526, PubMed=9165752;
 RA Leung J., Merlot S., Giraudat J.;
 RT "The Arabidopsis ABCISIC ACID-INSENSITIVE2 (ABI2) and ABI1 genes encode homologous protein phosphatases 2C involved in abscisic acid signal transduction";
 RL Plant Cell 9:759-771(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RA Rodriguez P.L., Grill E.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and YAC clones";
 RL DNA Res. 7:31-63(2000).
 CC -1- FUNCTION: INVOLVED IN ABCISIC ACID (ABA) SIGNALING PATHWAY.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
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 CC -----
 DR EMBL, Y08966; CAAT0163.1; -
 DR EMBL, Y08965; CAAT0162.1; -
 DR EMBL, Y118405; CAAT2538.1; -
 DR EMBL, AB024035; BAA97035.1; -
 DR HSSP; P35813; 1A60.
 DR InterPro; IPR001932; P2C-like.
 DR InterPro; IPR000222; P2C.
 DR Pfam; PF00481; P2C; 1.
 DR SMART; SM00331; P2C_Sig; 1.
 DR SMART; SM00332; P2C; 1.
 DR PROSITE; PS01032; P2C; 1.
 KW Hydroxylase; Manganese; Multigene family; Calcium-binding.
 FT CA BIND 70 81 EF-HAND (POTENTIAL).
 SQ SEQUENCE 423 AA; 46306 MW; 67CAACT6DA531A71 CRC64;

Alignment Scores:
 Pred. No.: 1,786-16
 Score: 333.00
 Percent Similarity: 44.91%
 Best Local Similarity: 29.28%

Length: 423
 Matches: 118
 Conservative: 63
 Mismatches: 130

Query Match: 13.01% Indels: 92
 DB: 1 Gaps: 19
 US-09-935-124A-1 (1-1422) x P2C2_ARATH (1-423)
 QY 252 CTCGCCACCCGCTAGC---AGTGGCATTCAGGT----- 281
 DB |||||
 QY 34 LeuProGluSerSerCysSerGlyAlaMetLysSerSerPheGluLeu 53
 DB |||||
 QY 282 -----TCTCTGCCCATCAATATCCAGATGGTAAAGATGAAAGGA 329
 DB |||||
 QY 54 ThrArgGlnSerSerLeuThrSerSerSerAlaMetAlaGlyValAsp----- 70
 DB |||||
 QY 330 GCMAAGAGMAAACCTCCGAGAGAGAGAGATGACAGTGAAGACTT----- 377
 DB |||||
 QY 71 -----LleSerAlaGlyAspGluLeuGlnGlySerAspGluPheAspProArgSer 87
 DB |||||
 QY 378 -----GTGAAAGAAAGTTGTAA-----GCCTCTGCGTATCTTGTGCTG 422
 DB |||||
 QY 88 MetAsnGlnSerGluLysLysValLeuSerArgThrGluSerArgSerLeuPhe 107
 DB |||||
 QY 423 AAGGCTAT-----GTGGCTAGCGGAGAGGAGGAGAGATGACAGAT 470
 DB |||||
 QY 108 LysCysValProLeuTyrglyValThrSerLecysGlyArgArgProGluMetGlyAsp 127
 DB |||||
 QY 471 -----GCCACGTCATCCTGAACGAC 491
 DB |||||
 QY 128 SerValSerThrIleProArgPheLeuGlnValSerSerSerLeuLeuAspGlyArg 147
 DB |||||
 QY 492 ATACCCGAGAGAGTGAAGCCCGCCATGTCCTCATTAATCGGGTTTCAATTTGCTGTT 551
 DB |||||
 QY 148 ValThrAsnGlyPheAsnProLysLeuSer-----AlaLysPheGluVal 163
 DB |||||
 QY 552 TTGTATGACATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 605
 DB |||||
 QY 164 TyzAspGlyLysGlyLysSerGlnValAlaMetLysCysValGlnArgMetLysLeuAla 183
 DB |||||
 QY 606 -----CAAACTTAATGAGAAATTTCTTAA-----GAGATGATATCAAGTGA 650
 DB |||||
 QY 184 LeuThrGluGluIleValLysGluLysProGluPheCysValAspGlyAsp-----ThrTyr 201
 DB |||||
 QY 651 GAGAAACCGTGAAGAGATGCTTTTGAACATTTGAACATTTGAACATTTGAACATTTGCTT 710
 DB |||||
 QY 202 GlnGluLysTyrLysLysAlaLeuPheAsnSerPheMetArgValAspSerGluLeu 221
 DB |||||
 QY 711 AAACAGCTCCAGCAGAAAGCTGCTGAAAGATGGGTGCACAGCGTGTTCG 770
 DB |||||
 QY 222 ThrValAlaLysAlaProGluThrVal-----GlySerThrSerValValAlaVal 238
 DB |||||
 QY 771 GCTGTAGACCAATCTTTATATTCGCAACCTCGAGATAGTCGGGCAATCTTGTGCTG 830
 DB |||||
 QY 239 ValPheProThrIleLysPheValAlaLysCysValAspSerArgAlaValLeuGlyAsp 258
 DB |||||
 QY 831 TATTAATGAGAGATCAAAACATGACAGCTTAAAGCTGACGAAAGATATATCAACT 890
 DB |||||
 QY 259 -----GlyLysThrProLeuAlaLeuSerValAspHisLysProAsp 272
 DB |||||
 QY 891 CAGTATGAAGAGCGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 941
 DB |||||
 QY 273 ArgAspAspGluAlaAlaArgLysGluAlaAlaGlyLysValIleArgTyrAsnGly 292
 DB |||||
 QY 942 GGGCGCTTTTGGCGCTGAGAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTG 1001
 DB |||||
 QY 293 AlaArgValPheGlyValLeuAlaMetSerArgSerLysGlyAsp-----ArgTyrLeuLys 311
 DB |||||
 QY 1002 TCGGCTGACCTCTGTGCGCGGACATCAAGAGCTGACAGCTGACAGCTGACAGCTGAC 1061
 DB |||||
 QY 312 ProSerValIleProArgProGluValThrSerValArgValLysGluLysAspCys 331
 DB |||||
 QY 1062 ATTTGTTGCTGCTGAGAGCTGCTTCAAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1121
 DB |||||
 QY 332 LeuIleLeuAlaSerAspGlyLeuThrAspValMetThrAsnGluGluValCysAspLeu 351


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Db      47 ProHieglyLeu---AspaNTPSerPhePheAlaValTyrAspGlyHisAlaGlySer 65
QY      573 CGAGCTCAAAATTTGCTGTCAGAGATTTGCATCAAACTTA-----ATC 617
Db      66 ArgValAlaIaenTyrCySerSerThrHisLeuLeuGluHisIleThrHisArgHisAlaPhe 85
QY      618 AGAAATTTCTCTAA---GGAGATGATC-----AGTGTAGAGAAACCGTGAAGA 668
Db      86 ArgAlaAlaAspYSerGlySerAlaLeuGluProSerValGlu---SerValYsThr 104
QY      669 TGCCTTTTGACACTTTCAAGCATCTAGAGATTCCTTAAACAGTTCACCGAG 728
Db      105 GlyIleArgThrGlyPheLeuYsIleAspGlyTyrMetArgHisPheSerAspLeuArg 124
QY      729 AAGCTGCTCGAAGATGGATGTCCTGCTGACGAGCTGCTGCTGCTGACCACTTCT 788
Db      125 AsnGlyMetAspArgSerGlySerThrHisAlaValGlyValMetValSerProThrHisMet 144
QY      789 TATATTGCCAAGCTCGAGATAGTCCGGCAATCTTGTGTGTTATATAGAGAGATCAA 848
Db      145 TyrPheIleAsnGlySerGlySerArgAlaValIleuGlyArgHisGln----- 161
QY      849 AAGATGCAAGCTTAAAGCTCAGCAAGATATATCAACTAGATATGAAGCGGATG 908
Db      162 -----ValCyAspSerThrHisAspHisLeuProCyAspHisProValGluYsGlu 178
QY      909 AGGATACAGAGAGCTGAGAGAAAGTCAAGGATGGCGTGTGGCGGCTGAGAGGTTG 968
Db      179 ArgIleGlnHisAspHisLeuGlySerValMetIleGlnHisGlyHisLeuAlaVal 198
QY      969 TCAGCTTCATTTGGGAGCGGCGAGTACAAAGCTGCGGT----- 1007
Db      199 SerArgAlaIleuGlyAspTyrAspTyrLeuValAspGlyYsGlyProThrHisGln 218
QY      1008 ----GTACCTCTGTGCTCCGACATCAAGCTGTCAGCTGACCCCAATGACAGTTCA 1064
Db      219 LeuValSerProGluProGluValTyrGluIleValAlaArgAlaGluGluAspGluPheVal 238
QY      1065 TTGTTGGCTGTGATGGGCTCTTCAAGGCTTACCCCAAGAGAGCGGATGATCATC 1124
Db      239 ValLeuAlaCyAspHisLeuGlyIleThrAspValMetSerHisGlnIleuGlyGluPheVal 258
QY      1125 TTGTCTGTCTCGAGATGAAAGATCCAGACCCGGAGAGGAAGTCCGAGCCGAGCC 1184
Db      259 LysSerArgLeuGlu-----ValSerAsp 266
QY      1185 CGCTACGAGAGAGCTGCAACAGGCTGCGCAACAGCGGCTGCGGCTGCGCGAC 1244
Db      267 AspLeuGluAsnValCyAspHisThrValAlaAspThrCysLeuHisLeuGlySerArgAsp 286
QY      1245 AACGTCACTGTATGGTGGT 1265
Db      287 AsnMetSerValValIleVal 293

RESULT 15
P2CB RAT ID P2CB RAT STANDARD: PRT: 390 AA.
AC P35815: 064046:
DT 01-UN-1994 (Rel. 29, Created)
DT 01-UN-1994 (Rel. 29, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (P2C-beta) (IA)
DE (Protein phosphatase 1B).
OS PM1B OR PM1B OR P2C2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=92201367; PubMed=1312947;

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RA Wenk J., Trompeter H.-I., Pettrich K.-G., Cohen P.T.W., Campbell D.G.,
RA Mieskes G.;
RT "Molecular cloning and primary structure of a protein phosphatase 2C
RT isoform.";
RL FEBS Lett. 297:135-138(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=95169115; PubMed=7532404;
RA Schaefer K., Braun T.;
RT "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+
RT dependent protein phosphatase beta.";
CC Biochem. Biophys. Res. Commun. 207:708-714(1995).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms, 1/Beta-1 (shown here)
CC and 2/Beta-MP; are produced by alternative splicing. Isoforms
CC appear to differ in their C-terminus.
CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
CC -----
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CC -----
DR EMBL: S90449; AAB21698.1; -.
DR EMBL: S74572; AAB33430.1; -.
DR PIR: S20392; S20392.
DR HSP: P35813; 1A60.
DR InterPro: IPR001932; P2C-1like.
DR InterPro: IPR000222; P2C.
DR Pfam: PF00481; P2C; 1.
DR SMART: SM00331; P2C SIG; 1.
DR SMART: SM00332; P2C; 1.
DR PROSITE: PS01032; P2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METRL 37
FT METRL 38
FT METRL 60
FT METRL 243
FT METRL 286
FT VASPLIC 379
FT FT
SQ SEQUENCE 390 AA; 42889 MW; D147615BC2FA140B CRC64;

Alignment Scores:
Pred. No.: 1.78e-15
Score: 319.00
Percent Similarity: 44.95%
Best Local Similarity: 29.36%
Query Match: 12.46%
DB: 1
Gaps: 9

US-09-935-124A-1 (1-1422) x P2CB_RAT (1-390)
QY 333 AGAGAAATTCCTCGAGAGAGAGATGCGAGTGTGAGAAAGAAAGTT 392
Db 7 LysProIleThrGluIleHisAsnAlaHisGlyAlaGluAsn----- 20
QY 393 TGTAAAGCTCTTCGATATCTTGTGCTGAAGGCTATGGCTGACCGAGAGGTGAG 452
Db 21 -----GlyLeuArgTyrGlyLeuSerSerMetClnGlyTyr 32
QY 453 AGGAGAGATGAGAGATGCCATCTCTGAAAGCATCAGCAGAGAGGTGAGGCC 512
Db 33 ArgValGluMetGluAspAlaHisThrAlaValAlaGlyIle----- 46

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QY 513 CCAATGCTCCATTAATCTGGGATTCATATTTGCTTTTATGACATGAGGAAAT 572
DB 47 PCHISGLYLEU--GLAASPTSPSPHERPHEALAVALLTYAASGLYHIALAGLYSER 65
QY 573 CGAGCTCAAAATTTGCTGCACAGAAATTCATCAAAACTTA-----ATC 617
DB 66 ARGVALALASNTYRCYSESTHRIELEULEUHNHILILETHThRANGLUAPHE 85
QY 618 AGAAATTTCTTAAGAGATGATATC-----AGTGAAGAGAAAACCGTGAGAGA 668
DB 86 ARGVALALASPLYSERGLYPHEALALEUGLUPROSERVALGLI--ASVALLYETHR 104
QY 669 TGCCCTTTGACACTTTCACATATACATGATAGAGAGTCTTAAACAGCTTCACAGCAG 728
DB 105 GLYILEARGTHRGLYPHELEULYSELASPLGLUTYMETARGASNPHESTERAPLEAUG 124
QY 729 AAGCTGCTCGGAAAGATGCGTCCATCGCTGCTTGTCTGTGATGACATATCTT 788
DB 125 AANGLYMETASPARISERGLYSETHRALVALGLYVALMETILESERPROTHRIASILE 144
QY 789 TATATTGCCAAGCTGCGAGATATGCGGCAATCTGTGCTTATATGAGAGAGATCA 848
DB 145 TYRPHIELAHNCYSELVAPSERHARGALVALLEUCYAHYDANGLYGIN----- 161
QY 849 AAACATGACAGCTTAAGCTTACGCAAGAACATATTCACATCAATGATGAAGCGGAT 908
DB 162 -----VALCYPHESERTHNGINASPHILELYSPICYASNPROMETGLULYSGLU 178
QY 909 AGGATACAGAGAGCTTGAGAGAAACGTCAAGAGTGGCGCTTTTGGCGCTTCAGAGTT 968
DB 179 ARGILEGLINASHLIGLYSERVALMETILEGLINARXVALANGLYSERLEUALVAL 198
QY 969 TCAAGCTCAATGGGAGCGGACAGTCAACAGCGCTGGCGT----- 1007
DB 199 SEVALGALALEUGLYASPLYRASYLYLYSCYVALASPLLYLYAGLYPROTHGLUGLN 218
QY 1008 ---GTCAAGCTCTGTGCCCCAGACATGACAGCGTGCACGTGACCCCAATGACAGGTTGAT 1064
DB 219 LEVALSERPROGLUPROGLIVALTYRGLIILELEUADRGALGLUGLADSPGLUPHEVAL 238
QY 1065 TTGTGGCTCTGATGGGCTCTCTCAAGGCTTTTACCCAGAGAGAGCGGTAACTTATC 1124
DB 239 VALLEUALICYAASPLGLYILETRAPVAPMETSEZASNGILUGLYLEUCYGLUPHEVAL 258
QY 1125 TTGTCTGCTGTCAGAGATGAAGATGACAGCCCGGAGAGGAGAGTCCGACGCGGACGCC 1184
DB 259 ASNPSEARXGLEUGLI-----VALSERAPR 266
QY 1185 CGCTAGAGAGAGAGCTGCGACAGAGCTGCGACAGAGCGGCTGACGCGGCTGCGCGGAC 1244
DB 267 ASPLLEUGLIASNTVALCYAHANTPRVALVALASPTHRCYULENHILYSELVASETHYDAPR 286
QY 1245 AAGCTCACTGATGCTGCTG 1265
DB 287 ASNPSESETHILEVALLEUAL 293

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RA Maeda T., Tsai A.Y.M., Salto H.;
RT "Mutations in a protein tyrosine phosphatase gene (PTP2) and a
RT protein serine/threonine phosphatase gene (PTC1) cause a synthetic
RT growth defect in Saccharomyces cerevisiae."
RL Mol. Cell. Biol. 13:5408-5417(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94254822; PubMed=8196609;
RA Robinson M.K., van Zyl W.H., Philizicky E.M., Broach J.R.;
RT "PTP1 of Saccharomyces cerevisiae encodes a protein phosphatase
RT 2C-like activity implicated in tRNA splicing and cell separation."
RL Mol. Cell. Biol. 14:3634-3645(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=5288c;
RA Andre B., Vissers S., Urrestarazu L.;
RL submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 167-281 FROM N.A.
RC STRAIN=5288c / AB972;
RA Murphy L., Richards C., Gentles S., Harrie D., Barrell B.G.;
RL submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IT HAS A SERINE AND A WEAK TYROSINE PHOSPHATASE ACTIVITY
CC WITH RATIOS OF SERINE TO TYROSINE PHOSPHATASE ACTIVITY AS HIGH AS
CC 200:1. IT IS ESSENTIAL FOR GROWTH OR GERMINATION AT 37 DEGREES
CC CELSIUS. MAY HAVE A ROLE IN THE HEAT SHOCK RESPONSE. INVOLVED IN
CC tRNA SPLICING AND CELL SEPARATION.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS. MANGANESE IS
CC ABOUT 20 TIMES MORE EFFICIENT THAN MAGNESIUM.
CC -1- SIMILARITY: BELONGS TO THE PTPC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L14593; AAA34920.1; -.
DR EMBL; Z48432; CAAB8353.1; -.
DR EMBL; Z74054; CAA98562.1; -.
DR EMBL; Z48008; CAA88055.1; -.
DR PIR; S41854; S41854.
DR HSSP; P35813; 1A60.
DR SGD; S0002164; PTC1.
DR InterPro; IPR001932; PTPC-like.
DR InterPro; IPR002222; PTPC.
DR Pfam; PF00481; PTPC_1.
DR SMART; SM00321; PTPC_Sig_1.
DR SMART; SM00321; PTPC_1.
DR PROSITE; PS01032; PTPC; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family; Heat shock.
FT METAL 36
FT METAL 37
FT METAL 37
FT METAL 58
FT METAL 233
FT METAL 272
FT METAL 272
FT CONFLICT 53
FT CONFLICT 124
SQ SEQUENCE 281 AA; 31549 MW; FA384D2541B20D50 CRC64;

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Alignment Scores:

Pred. No.:	2,116-15	Length:	281
Score:	317.50	Matches:	95
Percent Similarity:	45.87%	Conservative:	44
Best Local Similarity:	31.35%	Mismatches:	93
Query Match:	12.40%	Indels:	71
DB:	1	Gaps:	12

[illegible][illegible]

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RP SEQUENCE FROM N.A.
 Leung-Hagestedt Jn C., Mahendra A., Naruszewicz I., Hamigan G.E.;
 RA "Modulation of integrin signal transduction by ILKAP, a protein
 RT phosphatase 2C associating with the integrin-linked kinase, ILK1.";
 RL EMBL J. 0:0-0(2001).

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS;
 RA Struhsberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AL136850; CAB66784.1; -;
 DR EMBL, AY024365; AAK07736.1; -;
 DR EMBL, BC006576; AAK06576.1; -;
 DR HSSP; P35813; 1A6Q.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PRO0481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein; Kinase.
 SQ SEQUENCE 392 AA; 42906 MW; AF6AC98508CBEA3 CRC64;

Alignment Scores:
 Pred. No.: 1,28e-161 Length: 392
 Score: 2018.00 Matches: 392
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.83% Indels: 0
 DB: Gaps: 0

US-09-935-124a-1 (1-1422) x Q9H0C8 (1-392)

QY 102 ATGACCTCTTGGGGAGCTCCGAGAGCCGAGGCTCGCGGCGCGCTGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluArgSerProAlaAlaGlyLys 20
 QY 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCCGAGCAGTACTGACTCA 221
 DB 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 40
 QY 222 GATTCAGGGGAGACCTTGTCTTTGATGATCTCCACCCCTGACGAGCGCATTCAGGT 281
 DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProAlaSerSerGlyAspSerGly 60
 QY 282 TCTCTGGCCATCAATATCCGATGCTAAAGACTGAAGGAAAGGAAAGGAAAGAAA 341
 DB 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGluLysGlyAlaLysArgLys 80
 QY 342 ACCTCCGAGAGAGAGAAATGCGACATGAGAGACTGTGGAAAAGAAATTTGTAAGCC 401
 DB 81 ThrSerGluGluGluLysValSerGlnLysGluLysValGluLysValGlyLysVal 100
 QY 402 TCTTCGGTATCTTGTGCTGAAGGCTATGTGCTGAGCGGAAAGGTTGAGAGAGAG 461
 DB 101 SerSerValIlePheGlyLeuLysGlyLysValAlaGluArgLysGlyLysGluGlu 120
 QY 462 ATCAGAGATGCCACGCTCATCTGAGAGATGACGAGAGAGTGGAGCCCATGCTCC 521
 DB 121 MetGlnAspAlaIleValIleLeuAsnAspIleThrGluLysValGlyAspProPheSer 140
 QY 522 CTCATTAAGTGGGTTTCATATTTTGTGCTTTTGTGATGAGATGAGAGAAATTCAGCCTCA 581
 DB 141 LeuIleThrArgValSerLysPheAlaValPheAspGlyIleGlyIleAlaGlnAspSer 160
 QY 582 AAATTTGCTGACAGAAATTTGATCAAAATTAATCAAAATTTCTTAAGAGATGTA 641
 DB 161 LysPheAlaIleAlaGlnAsnLysGlnAsnLysIleArgLysPheProLysGlyAspVal 180
 QY 642 ATAGAGTGAAGAAACCGTGAAGAGATGCTTTTGAACATTTCAAGCATCTGATGAAGAA 701
 DB 181 IleSerValGluLysThrValLysValGlyCysLeuLeuAspThrPheLysShiIleThrAspGlu 200

QY 702 GAGTTCCTTAACAAAGCTTCCAGCCAGAAAGCTGCTGGAAAGATGGCTCCATGCCACG 761
 DB 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
 QY 762 TGTGTTCTGGCGTGTGAGACAACTTTTATTTGGCAACCTCGGAGATGTGCGGCAATC 821
 DB 221 CysValLeuAlaValAspAsnIleLeuLysIleAlaAsnLysGlyAspSerArgAlaIle 240
 QY 822 TTGTGCTTATTAATGAGAGAGATCAAAAACATGAGCCTTAAGCTTCAGCAAGAGCAT 881
 DB 241 LeuCysArgLysAsnGluLysSerGlnLysShiIleAlaLeuSerLeuSerLysGluHis 260
 QY 882 AATCAACTCAGTATGAGAGAGCGGATGAGATGACGAGAGCTGAGAGAAAGCTCAGGGAT 941
 DB 261 AsnProThrGlnLysGluLysArgLysGlnLysAlaGlyLysValAlaArgAsp 280
 QY 942 GGGCGGTGTTTGGGCGGTGTAGAGGTGACAGCTCATTTGGGAGAGCGGAGTAAAGCGCC 1001
 DB 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnLysArg 300
 QY 1002 TCGGGTCACTCTGTGCGCCGACATCAGACGCTGCGAGCTGACCCCAATGACAGATTTC 1061
 DB 301 CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
 QY 1062 ATTTGTTGGCTGTGATGAGGCTCTTCAAGTCTTTTACCCCAAGAAAGCCGTGAACCTTC 1121
 DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGluGluAlaValAsnPhe 340
 QY 1122 ATCTTGCTCTGTCTGAGAGATGAAGATCCAGACCCGGGAGAGGAAAGTCCGACCGGAC 1181
 DB 341 IleLeuSerCysLeuGluLysGlnLysIleGlnThrArgGlnLysSerAlaAlaAsp 360
 QY 1182 GCCCGCTACGAAGCAGACCTCGCAACAGGCTGCGCAACAAAGCGGTGACGCGGCTCGAGCC 1241
 DB 361 AlaArgLysGluAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgLysSerAla 380
 QY 1242 GACAACTCATCTGTATGTGTGTGCGGATGAGGCAAC 1277
 DB 381 AspAsnValThrValMetValValArgLysGlnHis 392

RESULT 2

Q8ROF6 PRELIMINARY PRT; 392 AA.
 ID Q8ROF6;
 AC Q8ROF6;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to protein phosphatase 2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Struhsberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026953; AAK26953.1; -;
 SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC9B7176 CRC64;

Alignment Scores:
 Pred. No.: 1,29e-154 Length: 392
 Score: 1935.00 Matches: 373
 Percent Similarity: 97.70% Conservative: 10
 Best Local Similarity: 95.15% Mismatches: 9
 Query Match: 75.59% Indels: 0
 DB: Gaps: 0

US-09-935-124a-1 (1-1422) x Q8ROF6 (1-392)

QY 102 ATGACCTCTTGGGGAGCTCCGAGAGCCGAGGCTCGCGGCGCGCTGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluArgAlaProArgProSerAlaGlyLys 20

[illegible]

QY	1242	GACCAACGCACTGATATGGTGGATGCGGATCGGCAC	1277
Db	381	AspernivalthralValmetValarglleglyHls	392
RESULT 3			
ID	Q9Z1Z6	PRELIMINARY:	PRT; 392 AA.
AC	Q9Z1Z6		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	
DE	Protein phosphatase 2C.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBITaxId=10116;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9074314; PubMed=9857069;		
RA	Tong Y., Quilston R., Shen S.H.;		
RT	"Cloning and characterization of a novel mammalian p2C isozyme.";		
RL	J. Biol. Chem. 273:35282-35290 (1998).		
DR	EMBL; AF095927; AAC97497.1; -		
DR	HSSP; P35813; 1A60.		
DR	InterPro; IPRO00222; P2C.		
DR	InterPro; IPRO01932; P2C-like.		
DR	Pfam; PF00481; P2C; 1.		
DR	SMART; SM00332; P2CC; 1.		
DR	SMART; SM00331; P2C; 1.		
DR	PROSITE; PS01032; P2C; 1.		
SO	SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;		
Alignment Scores:			
Pred. No.:	2,81e-154	Length:	392
Score:	1931.00	Matches:	373
Percent Similarity:	96.94%	Conservative:	7
Best Local Similarity:	95.13%	Mismatches:	12
Query Match:	75.43%	Indels:	0
DB:	11	Gaps:	0
US-09-935-124A-1 (1-1422) x Q9Z1Z6 (1-392)			
QY	102	ATGAGACCTCTTCGGGGAGACTGCGGAGCCGAGCCGCTGCGCGCCGCTCCGGGAAA	161
Db	1	MetAspleuPheGlyAspleuPheGluPProGluAsPProPProAsPProSeSeraIdIyls	20
QY	162	GAGGTCAAGAAAGAACCCCTGCTTTTGAATGACCTTCCTCGGCGACAGTACTGATCA	221
Db	21	GluAlaGlnGlnGluProValLeuPheGluAsPleuPProPProThrsSerSerThrAsper	40
QY	222	GGATCAGGCGGACCTTTCGTTTGAATGATCTCCACCCGCTAGCAATGSCATTCAGGT	281
Db	41	GlySerGlyGlyProLeuLeuPheAsPglyLeuPProPProIaGlySerGlyAsnSerIdyl	60
QY	282	TCTCTTCGCACATCATATTCGCCAGATGTTAAAGATCAAGAAAGAGCAAGAAAGAAA	341
Db	61	SerLeuAlaThrSerIdylSerGlnValValValAsnGlnGlyGlyGlyAlaLysArgys	80
QY	342	ACCTCCGAGAAAGAAAGAAAGCAAGCAAGCAAGCTTGAGAAAGAAAGTTGTTAAACC	401
Db	81	AlaPProGlnGlnGluLysAsnIdylGlyGlnLeuValGlnLysLysValCysLysAla	100
QY	402	TCTTCGGTATCTTTGGTCTGAAGGCTATATGCGCTAGACCGAAGGGTGAAGGAGAG	461
Db	101	SerSerValIlePheIdylLeuLysGlyLysValAlaGluLysGlyGlyLysGlyLysGly	120
QY	462	ATGCAAGATGCCACGTCATCTCTGAACGACATCCAGACCGAGAGTGTAGCCCATCTGC	521
Db	121	MetGlnAspAlaIleValIleLeuAsnAspIleThnGlnGlnLysAsnPProPProSer	140
QY	522	CTCATTAATCGGGTTTCATATTTTCTGTTTTTGAATGACATGAGGAAATTCAGACTCA	581
Db	141	IeuIleThrArgLysSerLysLysLeuAlaValPheAsPglyLysGlyLysIleArgLAser	160

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QY 582 AAATTGCTGCACAGAAATTGTCATCAAACTTAATCAGAAATTTCTTAAGGAGATGTA 641
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Db 161 LysPheAlaIaIeGlnIleuNleuHieGlnIleuNleuIleArgLysPheProIySglYAspVal 180
QY 642 ATCAGCTGTGAGAAAAACCGTGAAGAGATGCTTTTGACACTTTCAAGCATCTATGTGAA 701
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    |||
Db 181 IleSerValGlnLysThrValIySArgCysLeuLeuAspThrPheLysHieStrIAspGln 200
QY 702 GAGTTCCTTAACAAGCTTCCACGAGAGCCCTGGGAAAGATGGTCCATGTCACAG 761
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    |||
Db 201 GluPheLeuLysGlnIleAspSerGlnLysProIleTrpLysAspGlySerThrIleAlaThr 220
QY 762 TGTGTTCTGGCTGTAGACAACAATCTTTATTTATTTCCAACTTCGAGATAGTCGGGCAATC 821
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    |||
Db 221 CysValLeuAlaValIleAspIleuNleuTrIleAlaIleuNleuLysPheSerArgAlaIle 240
QY 822 TTGTGCTGTTATATAGAGAGAGTCAAAAACATGCAGCTTAAAGCTTCAAGCAAAAGCAT 881
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    |||
Db 241 LeuCysArgTyrAsnGlnLysSerGlnLysHieAlaAlaIleuSerLeuSerLysGlnHie 260
QY 882 AATCCAACTCAGATATAGAGAGCGATGAGATACAGAGGCTGAGAGAAACGTCAGGAGAT 941
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Db 261 AsnProThrGlnTyrGlnLysIleuArgIleGlnLysAlaIleLysIleAsnValIAsp 280
QY 942 GGGCGTGTGTTGGCGCTGTAGAGTGTCAAGCTCCATTTGGGAGCGGAGATCAAGCCG 1001
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Db 281 GlyArgValIleuGlnValIleuGlnValIleuSerArgSerIleGlyAspGlyGlnTyrLysArg 300
QY 1002 TGGGCTGTACCTCTGTGCGGACATCAAGCTGCCAGCTGACCCCAATGACAGCTTC 1061
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Db 301 CysGlyValIleuThrSerValIleuAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
QY 1062 ATTTGTTGGCGCTGTAGAGGCTCTCAAGGCTTTTACCACCAAGAGCGGAGATCTTC 1121
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Db 321 IleLeuLeuAlaIleCysAspGlyLeuPheLysValIlePheThrProGlnLysIleValIAsnPhe 340
QY 1122 ATCTTGCTCTGTCTCAGAGATGAAAAATCATCAGACCCGGGAGAGAGTCCGACGCGAC 1181
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    |||
Db 341 IleLeuSerCysLeuGlnLysArgIleGlnIleThrArgGlnLysIleProIleValIAsp 360
QY 1182 GCGCGCTGTAGAGAGCGCTGTGCAAGAGCTGTGCAAGAGCGGCTGTGCGGCTGCGCC 1241
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Db 361 AlaArgTyrGlnLysIleAlaIleCysAsnArgLeuAlaAsnLysHieIleValIleGlnArgIle 380
QY 1242 GACAAGCTCAGTGTGAGTGTGCGGATGAGGAGC 1277
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Db 381 AspAsnValIleThrValIleValIAspIleGlnHie 392

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RESULT 4

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Q9DC99 PRELIMINARY; PRT; 272 AA.
AC Q9DC99;
DT 01-0UN-2001 (TrEMBLrel. 17, Created)
DT 01-0UN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 0710007A1ARIK protein.
GN 0710007A1ARIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawata T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batistov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nikiyado I., Pesole G., Quackenbush J.,

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RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003007; BAB22508.1; -.
DR HSSP; P35813; 1A6Q.
DR MGD; MGI:1914694; 0710007A1ARIK.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 272 AA; 30279 MW; 465F2959D91BA63D CRC64;

Alignment Scores:
Pred. No.: 2,37e-108 Length: 272
Score: 1386.00 Matches: 266
Percent Similarity: 98.90% Conservative: 3
Best Local Similarity: 97.79% Mismatches: 3
Query Match: 54.14% Indels: 0
DB: 11 Gaps: 0

US-09-935-124A-1 (1-1422) x Q9DC99 (1-272)
QY 462 ATGCAAGATGCCAGCTCATCTGTAAGCAATCACCAGAGATGAGGCCCATCTGTC 521
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Db 1 MetGlnAspAlaIleValIleLeuAsnAspIleTrpGlnLysCysAsnProIleSer 20
QY 522 CTCATTACTCGGGGTTTCATATTGCTGTTTGTATGAGCATGAGGAAATTGAGCTCA 581
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Db 21 LeuIleThrArgValSerTyrPheAlaValIleAspGlyHieGlyIleArgIleAsp 40
QY 582 AAATTGCTGCACAGAAATTGTCATCAAACTTAATCAGAAATTTCTTAAGGAGATGTA 641
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Db 41 LysPheAlaIleGlnIleuNleuHieGlnIleuNleuIleArgLysPheProIySglYAspVal 60
QY 642 ATCAGCTGTGAGAAAAACCGTGAAGAGATGCTTTTGACACTTTCAAGCATCTATGTGAA 701
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Db 61 IleSerValGlnLysThrValIySArgCysLeuLeuAspThrPheLysHieStrIAspGln 80
QY 702 GAGTTCCTTAACAAGCTTCCACGAGAGCCCTGGGAAAGATGGTCCATGTCACAG 761
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Db 81 GluPheLeuLysGlnIleAspSerGlnLysProIleTrpLysAspGlySerThrIleAlaThr 100
QY 762 TGTGTTCTGGCTGTAGACAACAATCTTTATTTATTTCCAACTTCGAGATAGTCGGGCAATC 821
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Db 101 CysValLeuAlaValIleAspIleuNleuTrIleAlaIleuNleuLysPheSerArgAlaIle 120
QY 822 TTGTGCTGTTATATAGAGAGAGTCAAAAACATGCAGCTTAAAGCTTCAAGCAAAAGCAT 881
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Db 121 LeuCysArgTyrAsnGlnLysSerGlnLysHieAlaAlaIleuSerLeuSerLysGlnHie 140
QY 882 AATCCAACTCAGATATAGAGAGCGATGAGATACAGAGGCTGAGAGAAACGTCAGGAGAT 941
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Db 141 AsnProThrGlnTyrGlnLysIleuArgIleGlnLysAlaIleLysIleAsnValIAsp 160
QY 942 GGGCGTGTGTTGGCGCTGTAGAGTGTCAAGCTCCATTTGGGAGCGGAGATCAAGCCG 1001
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Db 161 GlyArgValIleuGlnValIleuGlnValIleuSerArgSerIleGlyAspGlyGlnTyrLysArg 180
QY 1002 TGGGCTGTACCTCTGTGCGGACATCAAGCTGCCAGCTGACCCCAATGACAGCTTC 1061
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Db 181 CysGlyValIleuThrSerValIleuAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 200

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QY 1062 ATTTGTGCTGTGATGGGCTCTTCAAGCTCTTTACCCCAAGAACGCTGAACTTC 1121
DB 201 11leuLeuAlaIaCysAspGlyLeuPheIysValPheIthrProGluGluAlaIaAsp 220
QY 1122 ATCTTGCTGTCTCGAGATGAAAGATCCAGACCCGGGAGGGAAGTCCGACCCGAC 1181
DB 221 11leuSerCysIleuGluAspAspIysIleGlnIthrArgIleGlyIysProAlaValAsp 240
QY 1182 GCCCGCTACGAGACGCTGCAACAGGCTGGCCCAACAGGCGGTGACGCGGGCTCGGCC 1241
DB 241 A1AaGlyTyrGluAlaIaIaCysAsnArgLeuAlaAsnIysAlaValAlaGlnArgIleSerAla 260
QY 1242 GACAACGTCACGTGATGATGGTGGTGGCGATAGGCGCAC 1277
DB 261 AspaenValThrValMetValValArgIleGlyHis 272

RESULT 5
Q9CS46 PRELIMINARY; PRT; 212 AA.
ID 09CS46;
AC Q9CS46;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 0710007A14R1k protein (Fragment).
GN 0710007A14R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shigaawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saio R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gasterich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzerelli J., Monbaerts P.,
RA Nordone P., Ringwald B., Ringwald N., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Botls A., Yoshida K., Hasegawa Y., Kawaji H., Kohenki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK019158; BAB31574.1; -.
DR HSSP; P35813; IAG6.
DR MGD; MGI:1914694; 0710007A14R1k.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
FT NON TER 1
SQ SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Alignment Scores:
Pred. No.: 2,11e-82 Length: 212
Score: 1078.00 Matches: 208
Percent Similarity: 99.06% Conserved: 2
Best Local Similarity: 98.11% Mismatches: 2
Query Match: 42.11% Indels: 0
DB: 11 Gaps: 0

US-09-935-124a-1 (1-1422) x Q9CS46 (1-212)

QY 642 ATCAGGTAGAGAAACCGTAGAGATGCTTTTGACACTTTCAGACATACATGATGA 701
DB 1 11leuSerValGluIysThrValIysArgCysIleuLeuAspThrPheIysThrAspGln 20
QY 702 GACTTCCTTAAACAAAGCTTCACGACGAGAACCTGGCTGGAAAGATGGGTCCATGGCCAG 761
DB 21 GluPheLeuIysGlnIleAspSerGlnIysProIleThrIlyAspGlySerThrIleAlaThr 40
QY 762 TGTGTCTGTGCTGTGACACATCTTTATATATTCGCAACCTCGGAGATAGTGGGCAATC 821
DB 41 CysValIleuAlaValAspAsnIleuIysIleAlaIleuGlyAspSerAlaIle 60
QY 822 TGTGTCTGTATATATGAGAGAGTCAAAACATCGACCTTAACTCACCACCAAGAGCT 881
DB 61 LeuCysArgTyrAsnGluGluIysSerGlnIysHisAlaIleuSerLeuSerIysGluHis 80
QY 882 AATCAACTCACTATGAAAGACGAGATGAGATGCAAGAGCTGAGAGAAACGTACGGAT 941
DB 81 AsnProThrGlnTyrGluGluIysArgMetArgIleGlnIysAlaGlyIysAsnValArgAsp 100
QY 942 GGGCGTGTGGGCGGTGCTAGAGTGTCAAGCTCCATGGGAGACGGCAGTCAAGCCG 1001
DB 101 GlyArgValIleuGlyValIleuGluValSerArgSerIleGlyAspGlyGlnTyrIysArg 120
QY 1002 TGGGATGACCTCTGTGCCCCGACATCAGACGCTGCGACGCTGACCCCAATGACAGGTT 1061
DB 121 CysGlyValIleuThrSerValProAspIleArgArgCysGlnIleuThrProAsnAspArgPhe 140
QY 1062 ATTTGTGCTGTGATGGGCTCTTCAAGCTCTTTACCCCAAGAACGCTGAACTTC 1121
DB 141 11leuLeuAlaIaCysAspGlyLeuPheIysValPheIthrProGluGluAlaIaAspPhe 160
QY 1122 ATCTTGCTGTCTCGAGATGAAAGATCCAGACCCGGGAGGGAAGTCCGACCCGAC 1181
DB 161 11leuSerCysIleuGluAspAspIysIleGlnIthrArgIleGlyIysProAlaValAsp 180
QY 1182 GCCCGCTACGAGACGCTGCAACAGGCTGGCCCAACAGGCGGTGACGCGGGCTCGGCC 1241
DB 181 A1AaGlyTyrGluAlaIaIaCysAsnArgLeuAlaAsnIysAlaValAlaGlnArgIleSerAla 200
QY 1242 GACAACGTCACGTGATGATGGTGGTGGCGATAGGCGCAC 1277
DB 201 AspaenValThrValMetValValArgIleGlyHis 212

RESULT 6
Q92072 PRELIMINARY; PRT; 167 AA.
ID Q92072;
AC Q92072;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 18.8 kDa protein (Fragment).
GN 0710007A14R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Stochard P.W., Pilgrim D.;
RT "Isolation of PP2C sequences using degenerate-oligo PCR.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBD databases.
DR EMBL; AF117831; AAD17234.1; -.
DR HSSP; P35813; IAG6.
DR MGD; MGI:1914694; 0710007A14R1k.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2EFB09D95B CRC64;

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Alignment Scores:

Pred. No.: 1,04e-63 Length: 167
 Score: 856.00 Matches: 165
 Percent Similarity: 99.40% Conservative: 1
 Best Local Similarity: 98.80% Mismatches: 1
 Query Match: 33.44% Indels: 0
 DB: 11 Gaps: 0

US-09-935-124A-1 (1-1422) x Q9ZMT1 (1-167)

QY 570 ATTCGAGCTCAAAATTTGCTGACAGAAATTTGATCAAAATTTATTCGAAAATTTCTT 629
 Db 1 TLeaTgAlaSerLyLeuAlaAlaGlnAenLeuHleGlnAenLeuIleArLySphePro 20
 QY 630 AAGAGGATGTATCTAGTGTAGAGAAAACCGTAGAGATGCTTTTGACCTTTCAAG 689
 Db 21 LysGlyAspRleIleSerValGluLysTrnValLysArgCysLeuAenAspTrnRheLys 40
 QY 690 CATACTGATGAAGAGTTCTTAAACAAGCTTCCAGCCAGAAAGCTGCGAAGATGGG 749
 Db 41 HleTrnAspGluGluPheLeuLysGlnAlaSerSerGlnLysProAlaTrpLysAspGly 60
 QY 730 TCCACTGCCACGTGTCTGCTGCTGACACACATTTCTTATTTATTCGCAACTCGAGAT 809
 Db 61 SerTrnAlaThrCysValLeuAlaValaAspAsnIleLeuTrpIleAlaAenLeuGlyAsp 80
 QY 810 ACTCGGGCAATCTGTGTGCTTATTAATGAGAGATCAAAAACATGCGCTTAAAGCTTC 869
 Db 81 SerTrnAlaIleLeuCysArgTrpAsnGluGluSerGlnLysHleAlaAenSerLeu 100
 QY 870 AGCAAAAGACATATTCACATCAGTATGAAGACGAGATGAGATACAGAGGCTGAGAGA 929
 Db 101 SerLySGluHleAenProThrGlnTrpGlnLysArgMetArgGlnLysAlaGlyGly 120
 QY 930 AACGTCAGGAGATGGCGTGTGTTGGCGCTTAAAGAGTGTACAGCTTCATTGGGACGGG 989
 Db 121 AenValaLysAspGlyArgValLeuGlyValaLeuGluValaSerArgSerIleGlyAspGly 140
 QY 990 CAGTCAACGCGTGGCGGTGCACTGTGCGCCGACATACAGAGCGTGCAGCGTCAACCCC 1049
 Db 141 GlnTrpLysArgCysGlyValTrnSerValProAspIleArgArgCysGlnLeuTrnPro 160
 QY 1050 AATGACAGGTTCAATTTGTTG 1070
 Db 161 AenAspArgPheIleLeuLeu 167

RESULT 7
 Q9ZMT1 PRELIMINARY; PRT; 341 AA.
 ID Q9ZMT1; AC Q9ZMT1; DT 01-OCT-2000 (TReMBLrel. 15, Created) DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update) DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update) DE T10F20.4 Protein. GN T10F20.4. OS Arabidopsis thaliana (Mouse-ear cress). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC Eurosid II; Brassicales; Brassicaceae; Arabidopsie. OK NCBI_TaxID=3702; RN SEQUENCE FROM N.A. RC STRAIN=CV. COLUMBIA; RA Sakano H., Liu S.X., Egu P., Lee J.M., Lenz C., Pham P., Toriumi M., Yu G., Chan A., Chung M., Goldemich A., Liu A., Smith A., Vaynsberg M., Alatefi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federpiel N.A., Theologis A.; RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1."; RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases. DR EMBL; AC034107; AAF97840.1; -.

DR HSBF, P35813; IABQ.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 SQ SEQUENCE 341 AA; 37367 MW; 6873C0CB82310195 CRC64;

Alignment Scores:
 Pred. No.: 5.75e-32 Length: 341
 Score: 481.00 Matches: 119
 Percent Similarity: 55.72% Conservative: 66
 Best Local Similarity: 35.84% Mismatches: 107
 Query Match: 18.79% Indels: 40
 DB: 10 Gaps: 11

US-09-935-124A-1 (1-1422) x Q9ZMT1 (1-341)

QY 333 AAGAGAAAACCTCCGAGAGAGAGAAATGCGACTGAAGCTTGTG----- 380
 Db 24 LysAlaLysLysSerGluGluValSerGlyGlyGluAlaValAlaAlaValGlyAen 43
 QY 381 ---GAAAGAAAGTTGTAAAGCCTTCGCGATC-----TTGGTGTG 422
 Db 44 ArgGluAlaGluGluAspLysProSerPheValSerGluGluLysLysGluPheLeuVal 63
 QY 423 AAGGCTATGTGCTGACCGGAGAGGTGAGAGGAGAGATGACAGATGCCACGTCATC 482
 Db 64 GluAlaAspValAlaGluAspLysGlyAlaArgHleTrnMetGluAspValTrpValVal 83
 QY 483 CTGAAGACATCACCGAGAGGTGAGGCCCATGTCCTCATTAATCTCGGCTTCATAT 542
 Db 84 LeuProAspAlaSerLeuAspPhe-----ProGlyTrnLeu-----ArgCysAlaHis 99
 QY 543 TTGCGTGTGTTTGAATGACATGAGAGAAATTCAGGCTCAAAATTTGCTGACAGAAATTTG 602
 Db 100 PheAlaIleTrpAspGlyHisGlyValArgLeuAlaAlaGluPheAlaLysLysHleu 119
 QY 603 CATCAAACTTAATAGAGAAAATTTCTTAAAGAGATGTATTCAGTGTAGAGAAACCGTG 662
 Db 120 HleLysAenValLeuSerAlaGlyLeuProArgGluLeuLeuAspVal---LysValAla 138
 QY 663 AAGAGATGCTTTTGACACATTTCAAGCATCTGATGAAGATTCCTTAAACAAGCTTCC 722
 Db 139 LysLysAlaIleLeuGluGlyPheArgLysTrnArgGluLeuLeuGlnLysSerVal 158
 QY 723 AGCCAGAAAGCGCTGGAAGAAGTGGTSCACTGCGAGTGTCTGAGTGTATAGAAC 782
 Db 159 Ser-----GlyGlyTrpGlnAspGlyAlaTrnAlaValCysValTrpIleLeuAspGln 176
 QY 783 ATTCTTATATTCGCAACCTCGAGATAGTGGCGCAATCTTGTCGT----- 830
 Db 177 LysValaPheValAlaAenIleGlyAspAlaLysValaValaLysSerSerThrTrn 196
 QY 831 -----TATTAAGAGAGAGTCAAAAACATGCAAGCTTTAAGCTTCAGCAAA 875
 Db 197 AenGluLeuGlyAenHleThrGluAlaGlyAenProLeuLysAlaIleValLeuThrArg 216
 QY 876 GAGCATATTCACATCAGATATGAAGGAGATGAGATATCAAGAGCGTGGAGAAAGTC 935
 Db 217 GluHleLysValaIleTrpProGlnIleLysSerArgIleGlnLysSerGlyValaIle 236
 QY 936 ---AGGATGGCGGTGTGTTGGCGCTGCTGAGAGTGTGACGCTCATTTGGGAGCGGAG 992
 Db 237 SerSerAenGlyArgLysGluGlnLysArgLeuGluValaSerArgAlaPheGlyAspArgHis 256
 QY 993 TACAAGCGCTGGGTGTACCTGTGCGCCGACATCAGACGCTGCGACGTGACCCCAAT 1052
 Db 257 PheLysLysPheGlyValaSerAlaThrProAspIleHleAlaPheGluLeuThrLysArg 276
 QY 1053 GACAGGTCATTTTGTGCGCTGTGATGGGCTTCACAGGCTTTTACCCAGAAAGCG 1112
 Db 277 GluAenPheMetIleLeuGlyCysAspGlyLeuTrpGluValaPheGlyProSerAspAla 296

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showmken R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sultson J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
 RA Waterson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."; (3)
 RL Nature 368:32-38(1994).
 RN
 RP SEQUENCE FROM N.A.
 RA Mortimore B.;
 RL Submitted (Nov-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL, Z81525; CAB04260.1; -.
 DR EMBL, AL031264; CAB04260.1; JOINED.
 DR EMBL, AL031264; CAB04260.1; -.
 DR EMBL, Z81525; CAB04260.1; JOINED.
 DR InterPro: IPR000232; P2C.
 DR InterPro: IPR001932; P2C-like.
 DR Pfam: PF00481; P2C; 1.
 DR SMART; SM00332; P2C; 1.
 DR PROSITE; PS01032; P2C; 1.
 SQ SEQUENCE 242 AA; 26845 MW; 62B6CA6104D34ADC CRC64;

Alignment Scores:
 Pred. No.: 2e-31 Length: 242
 Score: 474.00 Matches: 98
 Percent Similarity: 62.30% Conservative: 54
 Best Local Similarity: 40.16% Mismatches: 80
 Query Match: 18.52% Indels: 12
 DB: Gaps: 5

US-09-935-124A-1 (1-1422) x 062212 (1-242)

QY 345 TCCGAGAGAGAGAGATGGCAGTGAAGCTGTG-----GAAAGAAAGTT 392
 DB 3 SerAspSerArgLysArgSerSerAspPheU11eAspAsnSerArgLysLys 22
 QY 393 TGTAAAGCTCTTCGGTATCTTTGGTCTGAAGGCTATGTGCTAGCGGAAGGTAG 452
 DB 23 ProlYGLIserArgAsnLeuTyrCysThrLeuAlaIatryCysArgLysGLu 42
 QY 453 AGGAGAGATGCGAGATGCCCGCATCTGAAC-----GACATCACCGAGAGTGT 506
 DB 43 ArgAlaAspMetGlnAspThrHisIleMetLeuProlYpPheAspLeuGlyThrGlu-- 61
 QY 507 AGGCCCCCATCGCTCATCTACTGCGGTTTCATATTTGCTTTTGGAGACATGA 566
 DB 62 -----LysSerPheLeuSerArgAlaSerPhePheAlaIlePheAspGlyHisAla 78
 QY 567 GGAATTCAGAGCTCAAAATTTGCTGACAGAAATTTGCATCAAACTTAATCAGAAATTT 626
 DB 79 GlyProlArgAlaIleGlnHisCysGlnSerGlnMetGlyLysThrValLysGluLysLeu 98
 QY 627 CCTAAA---GGAGATGTAATCACTAGTGAAGAAACCGTGAAGAGTCCCTTTGACACT 663
 DB 99 AlaLysPheSerAspPheProlThrLeuThrLysSerLeuLysGlnThrPheThrGlnSer 118
 QY 684 TTCACACATACATGATGAGATGCTCTTAACCAAGCTTCCAGCAGCAGCTCGCTGAAA 743
 DB 119 TyrLysAlaValAspAspGlyPheLeuAlaIleAlaLysGlnAsnLysProlIleThrLys 138
 QY 744 GATGGCTCCACTGCCAGCTGTGTCTGCGTGTGACACAACTTTATATATGCAACTC 803
 DB 139 AspGlyThrThrIleThrIleMetIleIleLeuAsnAsnValIleTyrValAlaAsnIle 158
 QY 804 GGAAGATAGTGGGCAATCTTGTCTGTTATATGAGAGAGTCAAAACATGACGCTTA 863
 DB 159 GlyAspSerArgLysAlaValAlaArgLysLysGluAspLys---SerPheAlaProlVal 177
 QY 864 AGCTCAGCAAAAGATGATCCAGTCAAGAGAGAGAGTGAAGAGTGAAGAGAGCT 923
 DB 178 CysLeuThrValAspHisAspProlMetSerHisAspGlnArgMetArgIleGlnLysAla 197
 QY 924 GGAGGAAGCTCAGGAGATGGCGTGTGTTGGCGTGTGAGAGTGTACAGCTCATTTGG 983

DB 198 GlyAlaValValLysAspGlyArgIleAsnGlyValIleGlnLysSerArgSerIleGly 217
 QY 984 GAGCGGCACTACAGCGCTGCGGTGACCTCTGGGCCGACATGACAGCGCCAGCTG 1043
 DB 218 AspLeuProlPheLysSerLeuGlyIleIleSerThrProlAspLeuLysLeuThrLeu 237
 QY 1044 ACCCCCAATGAC 1055
 DB 238 ThrLysAsnAsp 241

RESULT 10
 Q8S820 PRELIMINARY; PRT; 319 AA.
 ID Q8S820;
 AC Q8S820;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Protein phosphatase 2C.
 GN MPC9.
 OS Mesembryanthemum crystallinum (Common ice plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
 NCBI_TaxID=3544;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Miyazaki S., Izumi S., Fukuhara T., Bohmert H.J.;
 RT "Plant Protein Phosphatases 2C ? A large protein family serving
 RT complex functions."
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AB083482; BAB88944.1; -.
 SQ SEQUENCE 319 AA; 34477 MW; 0BD28603E34CFB0 CRC64;

Alignment Scores:
 Pred. No.: 7.36e-26 Length: 319
 Score: 408.50 Matches: 113
 Percent Similarity: 54.04% Conservative: 41
 Best Local Similarity: 39.65% Mismatches: 86
 Query Match: 15.96% Indels: 45
 DB: Gaps: 12

US-09-935-124A-1 (1-1422) x Q8S820 (1-319)

QY 426 GGCTATGTGCTGAGCGGAGAGGATGAGAGATGACAGATGCCAGCTCATCTG 485
 DB 35 GlyTyr--AlaSerSerProGlyLysArgSerSerMetGlnAspPheTyrGluThrArg 53
 QY 486 AAGCAATCAGCAGAGAGTGTAGGCCCCCATGCTCCATTACTCGGGTTTCATATTT 545
 DB 54 IleAspGlyValGlnGly-----GluValValGlyLeuPhe 65
 QY 546 GCTGTTTGTGATGACATGAGAGAAATTCAGCTCAAAATTTGCTGCACAGAAATTTGCAT 605
 DB 66 GlyValPheAspGlyHisIleGlyValArgAlaIleGluTyrValLysGlnAsnLeuPhe 85
 QY 606 CAAACTTAATGAGAAATTTCTTAAGAGATGTATCAGGTGAGAAAACCGTGAAG 665
 DB 86 SerAsnLeuIle--LysHisProlYs-----PheIleSer-----AspThrLys 99
 QY 666 AGATGCTTTTGGACACTTTCAGACATCTGATGAAAGATTCCTTAACAGCTTCCAGC 725
 DB 100 SerAlaIleAlaGlnLysLeuTyrThrHisThrAspSerGlnPheLeuLysSerGlnAsnThr 119
 QY 726 CAGAGCTGCTCGAAGAT---GGGTCACTGCCACGTGTTCTGCGTGTAGCAAC 782
 DB 120 GlnAsn-----ArgAspAlaGlySerThrAlaSerThrAlaIleLeuValGlyAsp 136
 QY 783 ATTCTTTATATGCCAAGCTCGAGATGTGCGGCAATCTTGTCCTTATATAGAGAG 842
 DB 137 ArgLeuLeuValAlaAsnValGlyAspSerArgAlaValIleCysArgGlyGlyGlu--- 155
 QY 843 ACTCAAAACATGACGCTTAAGCTCAGCAAAAGACATATCCAACTCAGTATGAAG 902


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Db 156 -----AlaIleAlaValSerArgPheHisProAlaGlnSerArgGlu 170
QY 903 CGGATGAGATACAGAGGCTGAGAGAAAGCTCAGG-----GATGGCGCTGTTTG 953
Db 171 ArgGlnArgIleGluAspAlaGlyGlyPheValMetTrpAlaGlyThrTrpArgValGly 190
QY 954 GGGGTCTGAGAGGTTCACGCTCCATTGGGGACGGGACGATGCAAGCCCTCGGTGCACC 1013
Db 191 GlyValLeuAlaValSerArgPheAlaPheGlyAspLysLeuLeuLysGlnTyr--ValVal 209
QY 1014 TCTGTGCCCCGACATCAGACGCTGCAGTGAACCCCAATGACAGTTTCATTTGTTGGCC 1073
Db 210 AlaAspProGluIleGlnGluGluValValAspSerSerLeuGluPheLeuAlaLeuAla 229
QY 1074 TGTGATGGCTCTTCAGGCTCTTACCCCGAGAGAGAGCGGTGAACCTTCATCTGTCTGT 1133
Db 230 SerAspGlyLeuTrpAspValValThrAsnGluGluAlaValThrMetVal----- 246
QY 1134 CTCGAGAGATGAAAAGATCCAGACCCGGAGAGAGATCCGCGACGCCGCTACGAA 1193
Db 247 -----LysProIleGlnAspThr-----Glu 253
QY 1194 GCAGCTCGCAAGAGCTGCGCCACAAAGCGGTGCGAGCGGCTGCGCGACAAAGCTACT 1253
Db 254 GluAlaAlaLysLysLeuMetGlnGlnAlaTyrGlnArgGlySerAlaAspAsnIleThr 273
QY 1254 GTGATGTGTGTGCGG 1268
Db 274 CysValValValArg 278

RESULT 11
Q8RXV3 PRELIMINARY; PRT; 311 AA.
AC Q8RXV3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypochemical 33.2 kDa protein.
DE AT4G31750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_Taxid=3702;
RX [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carimaci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamliya A., Karlin-Neumann G., Kawai U., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.O., Sakurai K., Satou M.,
RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Becker U.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY080658; AAL86334.1; -.
KW Hypochemical protein.
SQ SEQUENCE 311 AA; 33247 MW; SE3098B91F116BFD CRC64;

Alignment Scores:
Pred. No.: 5,096-25 Length: 311
Score: 398.50 Matches: 112
Percent Similarity: 53.33% Conservative: 40
Best Local Similarity: 39.30% Mismatch: 88
Query Match: 15.57% Indels: 45
DB: 10 Gaps: 12

US-09-935-124A-1 (1-1422) x Q8RXV3 (1-311)
QY 426 GCGTATGTGCTGAGCGGAAGGCTGAGAGATGCGAGATGCCACGTCATCTCG 485
Db 35 GlyTyr--AlaSerSerProGlyLysArgSerSerMetGluAspPheTyr-GluThrArg 53

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QY 486 AAGACATCAGCCGAGAGATGAGGCCCCCATGCTCCTCATTAATCGGTTTCATATTT 545
Db 54 IleAspGlyValGluGly-----GluIleValGlyLeuPhe 65
QY 546 CGCTGTTTGAATGAGCATGAGAGAAATTCAGCCTCAAAATTTGGTCGACGAATTTGCAT 605
Db 66 GlyValPheAspGlyHisGlyGlyAlaArgAlaGlnIleValValGlnIleAsnLeuPhe 85
QY 606 CAAACTTAAATCAGAAATTTCTTAAGAGATGTAAATCAGTGAAGAAACCGTGAAG 665
Db 86 SerAsnLeuIleArg--HisProLys-----PheIleSer-----AspThrThr 99
QY 666 AGATGCCCTTTGAGACATTTCAACATATCTGATGAAGAGTTCTTAAACAGCTTCAGC 725
Db 100 AlaAlaIleAlaAspAlaTyrAsnGlnThrAspSerGluPheLeuLysSerGluAsnSer 119
QY 726 CAGAAAGCTGCTGGAAAAGAT--GGGTCCACTGCCAGCTGTGTGCTGTAGACAC 782
Db 120 GlnAsn-----ArgAspAlaGlySerThrAlaSerThrAlaIleLeuValGlyAsp 136
QY 783 ATTCTTAATATTCGAACCTCGAGATATGTGGGCAATCTTGTGCTTAATATGAGAG 842
Db 137 ArgLeuLeuValAlaAsnValGlyAspSerArgAlaValIleCysArgGlyGlyAsn-- 155
QY 843 AGTCAAAAACATGACAGCTTAAGCCTCAGCAAGAGACATATCAATCACTAGATGAAG 902
Db 156 -----AlaIleAlaValSerArgAspHisLysProAspGlnSerAspGlu 170
QY 903 CGGATGAGATACAGAGGCTGAGAGAAAGCTCAGG-----GATGGCGCTGTTTG 953
Db 171 ArgGlnArgIleGluAspAlaGlyGlyPheValMetTrpAlaGlyThrTrpArgValGly 190
QY 954 GGGGTCTGAGAGGTTCACGCTCCATTGGGGACGGGACGATGCAAGCCCTCGGTGCACC 1013
Db 191 GlyValLeuAlaValSerArgPheAlaPheGlyAspLysLeuLeuLysGlnTyr--ValVal 209
QY 1014 TCTGTGCCCCGACATCAGACGCTGCAGTGAACCCCAATGACAGTTTCATTTGTTGGCC 1073
Db 210 AlaAspProGluIleGlnGluGluValValAspSerSerLeuGluPheLeuAlaLeuAla 229
QY 1074 TGTGATGGCTCTTCAGGCTCTTACCCCGAGAGAGAGCGGTGAACCTTCATCTGTCTGT 1133
Db 230 SerAspGlyLeuTrpAspValValThrAsnGluGluAlaValThrMetVal-----LysAla 248
QY 1134 CTCGAGAGATGAAAAGATCCAGACCCGGAGAGAGATCCGCGACGCCGCTACGAA 1193
Db 249 IleGluAspPro-----Glu 253
QY 1194 GCAGCTCGCAAGAGCTGCGCCACAAAGCGGTGCGAGCGGCTGCGCGACAAAGCTACT 1253
Db 254 GluAlaAlaLysLysLeuMetGlnGlnAlaTyrGlnArgGlySerAlaAspAsnIleThr 273
QY 1254 GTGATGTGTGTGCGG 1268
Db 274 CysValValValArg 278

RESULT 12
Q8S3P1 PRELIMINARY; PRT; 243 AA.
AC Q8S3P1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypochemical 26.7 kDa protein.
DE 24K23.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_Taxid=39947;
RX [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN=CV. NIPPONBARE;
 RA Park Y.-J., Rostoks N., Ramakrishna W., Samiuel P., Shiloff B.,
 RA Ma J., Jiang Z., Kleinhofs A., Bennezen J.,
 RT "Sequence characterization of orthologous regions in the barley and
 RT rice genomes";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AF480497; AAL87187.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 243 AA; 26734 MW; 8B481E1F559CE5F CRC64;

Alignment Scores:

Pred. No.:	9 526-24	Length:	243
Score:	383.00	Matches:	99
Percent Similarity:	53.96%	Conservative:	44
Best Local Similarity:	37.36%	Mismatches:	78
Query Match:	14.96%	Indels:	44
DB:	10	Gaps:	8

US-09-935-124A-1 (1-1422) x Q8R3P1 (1-243)

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QY 534 GTTTCATATTTTCTGTTTGTGATGAGCATGAGAAATTCAGACCTCAAAATTTGCTGCA 593
DB 17 IIEGlyLeuphegLyValIheaprgLyHISgLyGlyAlaLyValaIaGlyUryValLyS 36
QY 594 CAGATTTGCATCAAAATTTATCAGA-----AAATTTCTTAAAGAGATGTAATCACT 647
DB 37 GlnAsnLeupheserHisLeuLeuArgHisProLySpheIleSerApThrLyValaIa 56
QY 648 GTAGAGAAAAACCGTGAAGAGATCCCTTTGGACACTTTCAGATCTGATGAAGGCTTC 707
DB 57 ILeuAp-----AspAlaTyrLysSerThrAspSerGluPhe 68
QY 708 CTTAAACAAGCTTCCAGCCAGAGACCTGCGTGAAGAGATGGCTCACTGCTGCTTT 767
DB 69 LeuGluSerAspSerSerGlnAsnGlnCyS-----GlySerThrLysSerThrAla 85
QY 768 CTGGCGCTGACACACATTCTTATATTCACACCTCGAGATAGTCGGCAATCTGTGT 827
DB 86 ValLeuValaGlyAspArgLeupheValaIaAsnValaGlyAspSerArgAlaIleIleCyS 105
QY 828 CGTTTAAATGAGAGAGAGTCAAAAACATGCACCTTAAGCCTCGCAAAAGCATATTC 887
DB 106 ArgGlyGlyAsn-----AlaIleAlaValSerLysAspHisLysPro 119
QY 888 ACTCATGATGAGAGCGGATGAGATACAGAGCGTGAAGAAACGTCAAG----- 938
DB 120 AspGlnThrAspGlnArgGlnArgIleGluAspAlaGlyGlyPheValaIaMetTrpAlaGly 139
QY 939 GATGGCGCTGTTTGGCGCTGCTAGAGGTGTCAAGCTCAATGGGAGCGGCGATACAG 998
DB 140 ThrTrpArgValaGlyGlyValaIleuAlaValaSerArgAlaPheGlyAspLysLeuLeuLys 159
QY 999 CGCTGCGGTGTCACTCTGTGCGCCGACATCAGACGCTGCAGCTGACCCCAATGACAG 1058
DB 160 GlnTyrValaValaAsp---ProGluLysArgGluGluValaIleAspHisSerLeuGln 178
QY 1059 TTCAATTTTGTGGCGCTGTGAGGCTCTTCAAGCTTATCCCAAGAAAGCGCTGAC 1118
DB 179 PheLeuIleLeuAlaSerAspGlyLeuTrpAspValaValaThrAsnGluGluAlaValaAsp 198
QY 1119 TTCAATCTTCTCTGTCTGAGATGAAGAAATCAGACCCGGAGAGGAAGTCCGACGCC 1178
DB 199 MetThrArgSerLysIleHisAspProGluGlu----- 208
QY 1179 GACGCCCGCTACAGACACCTGCAACAGGCTGCGCAACAGCGGCGCTGCG 1238
DB 209 -----AlaAlaLysLysLeuGlnGluAlaLysLysArgGluSer 222
QY 1239 GCCGACAACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
DB 223 SerAspAsnIleThrCysValaValaValaArgPheLeuHis-----GlyGln 237
QY 1299 GAGCAGCATGTGTAT 1313

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DB 238 GlySerSerGlyTyr 242

RESULT 13

ID Q8RX37 PRELIMINARY; PRT; 380 AA.

AC Q8RX37
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 40.7 kDa protein.

GN ATIG07160.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 NC NCBI_TaxID=3702;

RM [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C.C., Tortum M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Chen H., Cheuk R., Jones T., Karlin-Neumann G., Kim C., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Nguyen M., Palm C.J., Shim P.,
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RT "Arabidopsis Open Reading Frame (ORF) Clones";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY090917; AAM13912.1; -;
 KW Hypothetical protein.

SQ SEQUENCE 380 AA; 40709 MW; 7EA1DB8B91F0E8BD CRC64;

Alignment Scores:

Pred. No.:	7e-23	Length:	380
Score:	373.50	Matches:	125
Percent Similarity:	42.20%	Conservative:	59
Best Local Similarity:	28.67%	Mismatches:	140
Query Match:	14.59%	Indels:	112
DB:	10	Gaps:	17

US-09-935-124A-1 (1-1422) x Q8RX37 (1-380)

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QY 14 CTGCTCCGCGCCCGCGGGGCTGTGAGCCCGCGCTGCTGCGGCGCTGAC-----TGT 67
DB 41 LeuAsnProProValSerSerThrSerProSerAlaIaAspProThrSerProPheCyS 60
QY 68 CTGTGCTGCTGCGCGCTCCACCGACCTCGGCATGAGACCTTCGGGAGCTGCGCG 127
DB 61 LeuArgLeuLeuLysProProAlaLysLeuGlyPheGlySerAspSerGlyProGlySer 80
QY 128 GCCCGAGCGCTGCGCGCGCGCGCTGCGCGGAGAGAGCTCAGAAAGACCCCTGCTTT 187
DB 81 IleLeu-LysArgLysArgLysProThrThr----- 89
QY 188 TGATACCTCCTCCTCGCGCGACGATGACTGACTCAGAGATCAGGAGGACCTTGTCTTTGA 247
DB 90 -LeuAspIleProValaIa-----ProValGlyIleAlaIaProIleSerAsnAl 106
QY 248 TGATCTCCACCGCGCTGACAGTGGGATTCAGGTTCTTGGCAATCAATATCCAGAT 307
DB 106 AspThrProArgGluGlu-----SerArgAl 115
QY 308 GGTAAAGCTGAAGGAGAAAGAGCAAAAGAAAGAAACCTCCGAGAGAGAGAAATGCGAG 367
DB 115 aValGluArgGluGlyAspGly----- 122
QY 368 TGAAGAGCTTGTGAGAAAGAAAGATTGTGAAGCTCTTCGATGATCTTGTGTAAGGG 427
DB 123 -----TyrSerValTyrCysLys----- 128
QY 428 CTATGTGCTGAGCGGAAAGGCTGAGAGAGAGAGATGAGATGCGCACTGATCTGAA 487
DB 129 -----ArgGlyLysArgGluAlaMetGluAspArgPheSerAlaIleTh 143

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OY 488 CGACATCACCGAGAGTGTAGCCCGCATGCTCCCTATTACTGCGGTTTCATTTTGC 547
Db 143 rñenleuGInglyaap-----ProlysglnAlaIle-----PheG1 155
OY 548 TGTGTTTGTATGATCGATGAGAAATTCAGGCTCAAAATTTGCTGCACAGATTGTGATCA 607
Db 155 yValIYrAepG1yAInglyGlyrProthrAlaIaGlnPheAlaIaLysAaenleuCyhIs 175
OY 608 AAATTAATTCAGAAAAATTTCTTAAGAGATGTATTC-----AGTGT 649
Db 175 rñenleuLeu-----GlyGlnleValIglyIaYrAenGlnserLyse11 190
OY 650 AGAGAAACCGTGAAGAGATGCTTTTGAACCTTTCAACATCTGATGTAAGATTCTT 709
Db 190 eGIuGlnIaValIyAaYsglyYrLeu-----AlatrAepserGIuPhele 206
OY 710 TAAACAAGCTTCACCGACGAAAGCTGTGAAAGATGGGTGCACATGCGACAGTGTCTT 769
Db 206 ulYsgIuYrAaenVal-----LysGIyGIyserCySValThrAlaLe 221
OY 770 GGCCTGTAGCAACATTTCTTTATTTGCGCAACCTCGAGATGATCGGCAATCTGTGTG 829
Db 221 uIleSerAepGIyAaenleuValIaIaAaenAlaGIyAaPcyAaYgAlaValleu----- 239
OY 830 TTATATATGAGAGATGCAAAACATGCAAGCTTAAGCTTCACGCAAAAGCATATTCGAAC 889
Db 240 -----SerValGIyGIyPheAlaGIuAlaLeuThrSerAaPcyAaYgProse 255
OY 890 TCAATATGAAAGCGGATGAGATACAGAAAGCTGTGAGGAAACGTCAAGAT----- 941
Db 255 rAysAaPepGIuAaYgAaenAlaYglleGIuSerseGIyYrValAaPthrPheAaen 275
OY 942 ----GGGCTGTTTGGCGGTGCTTGAAGGTGTCAAGCTTCATTTGGGGAAGCGGATGACAA 997
Db 275 rValIYrAaYglleGIuYrleuAlaValaIaSerAaYgIyIleGIyAaPAlaHIsleuLy 295
OY 998 GCGCTCGGATGTACCTCTGTGCCGATCAGACGCTCAGCTGACCTGACCCCAATGACAG 1057
Db 295 sGln-----TyrIleIleSerGIuProGIuIleAaenIleuAaYglleAaPProGIuHIsGI 314
OY 1058 GTTCATTTTGTGGCTGTGATGGGCTCTTCAAGGTCTTTTCAAGCCGAGAAAGGCGCTGAA 1117
Db 314 uPheleuIleuAlaIaSerAaPcyYrleuTyrAaPlyrValaIaSerAaenGIuAlaValaIs 334
OY 1118 CTTTCATCTTGTCTGTCTGTGAGATGAAAGATCCAGACCCGGAAGGAGATGCCGAGC 1177
Db 334 pIle-----AlaAaYrPheCySlysglyTh 343
OY 1178 CGAGCGCGGCTACGAA-----GCAGCTGTGCAAGGCTGTGCGCAACAGGGGTGACAGC 1231
Db 343 rAaPgluYrAaYgIyPProleuIleuAlaCySlySlySleuValaIaPleuSerValaIaSerA 363
OY 1232 GGGCTGGCGGCAAGATCAGCTGTGATGCTGTGCGGATGAGGCGAC 1277
Db 363 gGIySerleuAaPepIleSerValaIeIuIleGIuIleuCyhIs 378

RESULT 14
OBYVZNS
ID OBYVZNS PRELIMINARY; PRT; 371 AA.
AC OBYVZNS;
DT 01-MAR-2002 (TRMBLrel. 20, Created)
DT 01-MAR-2002 (TRMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
DB HYPOthetical 40.6 KDa protein.
GN AT1G43900.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

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RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carlini P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ihida U., Jones T., Kamiya A., Katlin-Neumann G.,
RA Kawai U., Kim C., Kosemura E., Lam B., Lin J., Meyers M.C., Mienda M.,
RA Narusaka M., Nguyen M., Palm C.U., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinzaki K., Davis R.W., Becker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At1g43900 (GI:15218577).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY063973; AAL36329.1; -.
DR InterPro; IPR001932; P2C-1.
DR InterPro; IPR00481; P2C; 1.
DR Pfam; PF00481; P2C; 1.
DR SMART; SM00332; P2C; 1.
DR PROSITE; PS01032; P2C; UNKNOWN_1.
KW Hypothetical protein.
SQ
SEQUENCE 371 AA; 40582 MW; 5579D3D23F1805B8 CRC64;

Alignment Scores:
Pred. No.: 1,376-22 Length: 371
Score: 370.00 Matches: 120
Percent Similarity: 45.27% Conservative: 62
Best Local Similarity: 29.85% Mismatches: 117
Query Match: 14.45% Indels: 103
DB: Gaps: 17

US-09-935-124A-1 (1-1422) x OBYVZNS (1-371)
OY 80 CCGCTTCACCCAGCTCCGCAATGACATCTTTGGGAGACTGCCGAGCCGAGCGCTC 139
Db 64 ProserProProProleuSerValaIaProleuYrGIyAaPAlaAaenSer----- 80
OY 140 GCGCGCCCGCGCTGCGGGAAGAAAGCTCAGAAAGACCCCTGCTTTGATGACTCCG 199
Db 81 -----Pro-Pr 82
OY 200 TCCGCGCAGAGTACTGACTCAGATCAGGAGACCTTTGATGATGATCTCCAC 259
Db 82 oProGIuIleSerSerSerProAlaThrLySerSerleuMeIle----- 97
OY 260 CGTAGACAGTGGGATTCAGTTCTCTTGCACATCAATATCCAGANTGTAAAGACTGA 319
Db 98 ----SerSerAaYrAaPProAaenAlaIeupHeserGIy----- 108
OY 320 AGGGAAGAGAGCAAGAAAGAAACCTCCGAGAGAGAAAGATGCGAGTGAAGACTGT 379
Db 109 -----GlyGIyIleSerPheAlaI 115
OY 380 GGAAGAAAGATTGTAAAGCTCTTGGTGATCTTGTGTGAAGGGCTATGTGCTGA 439
Db 115 aGIyValaYrThValaYrPheSer-----TyrGIyYr-----SerSe 128
OY 440 GCGGAAGGTGAGAGAGAGAGATGACAGAT--GCCACGTATCTGTAAAGATACAC 496
Db 128 rleuYrGIyYrAaYrAlaIaThrMeGIuAaPlyrPheGIuThAaYrIleSerAaPValaIs 148
OY 497 CGAGAGTGTAGGCCCCCATGCTCCCTCATTAATCTGCGGTTTCATATTTGCTGTTTGA 556
Db 148 nGIyGln-----MetValaIaPhePheGIyValaIaPheAs 159
OY 557 TGAACATGAGAGATTCAGAGCTCAAAATTTGCTGCACAGATTTGCATCAAACTTAAT 616
Db 159 pGIyHIsGIyGIyAlaYrAlaYrThAlaGIuYrleuYrAaenAaenleuPheIyAaenleuVa 179
OY 617 CAGAAAAATTTCTTAAGAGATGTATCATGTGTAGAGAAAAACGTAAGAGATGCTTTTGA 676
Db 179 I-----SerHIsAaPpPheIleSer-----AspThrLyValaIaIleVa 193
OY 677 GGAACATTTCAACATATCATGATGAAGATGCTTT--AAACAAGCTTCACGAGAAAGCC 733
Db 193 IGIuValaPheIyGIuThrAaPgluGIuYrleuIleGIuGlnIaGIyGIuIleProLyAaIs 213
OY 734 TGCGTGAAGAAAGATGGGTCACTGCAAGTGTGTTCTGCTGTGTGACAAATCTTTATAT 793

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Db 213 nlaa-----GlySerThrAlaAlaThrAlaPheLeuIleGlyAspLysLeuIleVal 230
Qy 794 TCGCAACCTCGAGATAGTGGGCGCATCTGTGCTTAATATGAGAGCAAAACA 853
Db 230 lalaenvaliglyaspserrhryvala-----AlaSerArgencl 244
Qy 854 TCGAGCTTAAGCTCAGCAAAAGCATATTCACACTCAGATGAAGCGGATGAGAT 913
Db 244 yerralaValProLeuSerAspaphilLysProAspArgSerAspGluArgIlnArgI 264
Qy 914 ACAGAAAGCTGAGGAAAGCTC-----AGGATGGCGCTGTTGGCGCTGTAA 964
Db 264 egluapalaglygylPheIleIleThrPalaglyThrTrpArgValGlyGlyIleLeuAl 284
Qy 965 GGTGTCACCTCATTTGGGACGGGAGTAGACAAGCGCTGGGTGTCACCTGTGCGCG 1024
Db 284 aValSerArgAlaPheGlyAspLysGlnLeuLysProLysr--ValIleAlaLupProG 303
Qy 1025 CATCAGACGCTGCGACGCTGACCCCAATGACAGGTTCAATTTGGCTGTGATGGCT 1084
Db 303 ulleaglIngluLapIleSerThrLeuGlu---PheIleValAlaSerAspGlyLe 322
Qy 1085 CTTCAAGCTCTTATCCCGCAGAGAACCGTGAACTTCTCTTCTCTGTCGAGATGA 1144
Db 322 urTrpAsnValLeuSerAsnLysAspAlaValAlaIleVal----- 335
Qy 1145 AAAGATCCAGACCGGGAGAGGATCCGACCGGACCGCTACAGACGCTGCAA 1204
Db 336 -----ArgAspIleSerAspAla-----GluThrAlaAlaAr 346
Qy 1205 CAGGCTGCGCAACAGCGGCTGCGAGCGGCTGCGCGACAGCTGATGATGGTGT 1264
Db 346 glylsleuValGlnGluGlylTyralaArgLysSerCysAspAsnIleThrCysIleValVal 366
Qy 1265 GCGG 1268
Db 366 lArg 367

RESULT 15
015743 PRELIMINARY; PRT; 975 AA.
ID 015743;
AC 015743;
DT 01-JAN-1998 (TRMBLrel. 05, Created)
DT 01-JAN-1998 (TRMBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
DE Spalten.
CN SPAN.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=98252837; PubMed=9585512;
RA Aubry L., Firtel R.A.;
RT "Spalten, a protein containing Galpha-protein-like and Ppzc domains,
is essential for cell-type differentiation in Dictyostelium.";
RU Genes Dev. 12:1525-1538(1998).
DR EMBL; AF019985; AAB70844.1; -.
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR001019; Gpocotin_alpha.
DR InterPro; IPR000222; Ppzc.
DR InterPro; IPR001932; Ppzc-like.
DR Pfam; PF00503; G-alpha; 1.
DR Pfam; PF00481; Ppzc; 1.
DR ProDom; PD00281; Gpocotin_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
DR SMART; SM00332; Ppzc; 1.
DR SMART; SM00331; Ppzc_Sig; 1.
DR PROSITE; PS01032; Ppzc; 1.
SQ SEQUENCE 975 AA; 109016 MW; BBB322F5026D2A4F CRC64;
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Alignment Scores:
Pred. No.: 1,89e-22 Length: 975
Score: 370.00 Matches: 126
Percent Similarity: 41.03% Conservative: 57
Best Local Similarity: 28.25% Mismatches: 164
Query Match: 14.45% Indels: 99
DB: 5 Gaps: 19

US-09-935-124A-1 (1-1422) x 015743 (1-975)
Qy 5 CCAGGCCGCGCTGCGCGCGCGCGCGGAGCCCGCGCGCTGCTCGCGGCTGAG 64
Db 599 ProLysProValLysProLysGluProLysProLysGlu----- 613
Qy 65 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
Db 614 -----ProLysProLysGlu-----Pr 620
Qy 125 GGAGCCCGAGCGCTGCGCGCGCGCGCGCGGAGAGAGCTCAGAAAGACCCCTGCT 184
Db 620 olvsProLysGluProLysProLysProLysProLysProLysProLysProVally 638
Qy 185 CTTTATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 244
Db 638 b---GluSerLysProProLysGlu----- 645
Qy 245 TGATGATCTCCAGCCGCTAGCAGTGCGGATTCAGGTTCTTTCGACATCAATATCCA 304
Db 646 -----ProLysProLysGluProLysGluSerLysGluProLysGluProLys 662
Qy 305 GATGTTAAAGACTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 347
Db 662 sgluProLysProThrLysProProLysGluLysLysThrSerLysValAspGlyAlaI 682
Qy 348 -GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 394
Db 682 agluSerLysLysAsnGlyAlaAspSerCysglYanGlyValGlySerLysIleLys 702
Qy 395 TAAAGCTCTTCTGATGATCTTGTGCTGAGAGGCTATGCTGCTGCGGAGAGGTGAG 454
Db 702 bleuGluSerGly-----PheGly-----SerLeuGlnGlyArgAr 714
Qy 455 GGAGAGAGATGAGATGCCAGCTCATCTTGAACGACATCACCGAGAGGTGAG- 509
Db 714 glyAsnMetGluAspThrHisValIleLeuAsnMetGluAlaValThrTyAs 734
Qy 510 -----CCCCATGCTCCCTCATTAATCTCGGCTTCAATTTGCTGTTTGAAGCATG 565
Db 734 nglyProProLysAspIle-----ProIleSerTyTyralaValTyAspGlyHisG 752
Qy 566 AGGAATTCGAGGCTCAAAATTTGTCACAGATTTGCATCAAACTTAATC-----AG 619
Db 752 yGlyThrGluThrSerThrLeuGluProThrValHisAsnGlySerValAsnSerG 772
Qy 620 AAAATTTCTTAAAGAGATGTATCATGTAGAGAAAACGTTGAAGAGATGCTTTTGA 679
Db 772 nserHeArgAspGlyAsp-----TyGluGlnAlaPheArgAs 785
Qy 680 CACTTCAAGCATCTATGATGAAGATTCCTTAACAGACTTCACCGCAGAACCTGCTG 739
Db 785 palatYrAlaGluAlaAspAspIleValIleGluLysCysGlu----- 799
Qy 740 GAAAGATGGGTCACTGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
Db 800 -LysSerGlySerThrGlyValSerAlaLeuValGlyValGlyValGlyValGlyVal 819
Qy 800 CTTGAGATAGTCCGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
Db 819 nValGlyAspSerGluIleValAlaArgAlaGlnProAsnAlaAsnProLysGlyPr 839
Qy 860 CTTAAGC-----CTAGCAAGAGCATATCACTCACTGATGAAGAGCG 904
Db 839 ovalThrTyGluProValLeuLeuSerTyLysHisLeuAlaSerAspAspGlnGlu 859
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QY 905 GATGAGATACAGAAAGCGTGGAGAAAGCTCAGAGATGCGCTGTTTGGCGGTCTAGA 964
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 859 elysarlgvalthrlepleuileglymetillelephenalaigleupheglserrleua 879
QY 965 GGTGTACGCTCATTTGGGAGCGGACAGTCAAGCCC-----TCCGCTGT 1009
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 879 avalsarlgserpneglyasplyslylrylsuylgylulyslyblyphecys---- 897
QY 1010 CACCTCTGCGCAGATCAGACCGTCCAGCTGACCCCAATGACAGTTTCATTTGTT 1069
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 898 -valseraspprolyrglnthrthrthrlepleuilealargasphlspherillele 917
QY 1070 GCGCTGTGATGGCTCTTCAAGTCTTTACCCCAAGAAAGCCGTGAATTCATCTTGTG 1129
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 917 ualaCyaspglyleuphrasplysvalglulryaspglualavalalnphenale----- 935
QY 1130 CTGTCTCGAGATGAAAGATCCAGACCCGGAAGGAAAGTCCGAGCCGACCGCTGA 1189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 936 -----GlnArganillelyleuglylserserlathrglu----- 947
QY 1190 CGAAGCAGCTGCAACAGGCTGCGCAACAGCGGTGCGAGCGGCTCGGCGCAACGT 1249
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 948 -----IlesergluleuleuAlaGlnaspseryraspharglserserglyasphani 965
QY 1250 CACTGTGATGGTGTG 1265
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 965 ethrvalleuvalval 970

RESULT 16
Q8VZD9 PRELIMINARY; PRT; 420 AA.
ID Q8VZD9
AC Q8VZD9;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE AT5953140/MFH8.8.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koeseema B., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang B., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Nurusaki M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seti M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Becker J.R.;
RT "Arabidopsis cDNA clones.", EMBL/GenBank/DBJ databases.
RU Submitted (NOV-2001) to the
EMBL, AIO65026; AAL57666.1; -.
DR InterPro: IPR000222; PF2C.
DR InterPro: IPR001932; PF2C-1like.
DR Pfam: PF00481; PF2C; 1.
DR SMART: SM00332; PF2C; 1.
DR SMART: SM00331; PF2C; 1.
DR SMART: SM00332; PF2C; 1.
DR PROSITE: PS01032; PF2C; UNKOWN.1.
SQ SEQUENCE 420 AA; 45752 MW; 2DF6960D75BF9058 CRC64;

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Alignment Scores:

Pred. No.:	1,91e-22	Length:	420
Score:	368.50	Matches:	112
Percent Similarity:	50.44%	Conservative:	60
Best Local Similarity:	32.84%	Mismatches:	108
Query Match:	14.39%	Indels:	61
DB:	10	Gaps:	13

US-09-935-124a-1 (1-1422) x Q8VZD9 (1-420)

```

QY 291 ACATCATATCCAGATGTGTAAGACTGAAAGGAAAGCAAAAGAAAGAACTCCGAG 350
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 Thiersalalysermetelvalaspthr-----Serlealely 69
QY 351 GAAAGAGAAAGATGCACTGAAAGAGCTTGGAAGAAAGAAAGTTGTAAAGCTTCCTG 410
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 GlnulysarglleserleuvalasphmetProbidulysvalasphapolylytrylle 89
QY 411 ATCTTGCTGTGAAG-----GCTATGTGCTGAGCGGAG 446
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 glylgllylrylsasnasphasplyserleuserCyseidlytryCyserhearg-- 108
QY 447 GGTGAGAGGAGAGATGACAGAGATGCCAGCTCATCTGAACACATCCAGAGAGTGT 506
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 109 Glylsarlgserthrmetglulaspheyrasphlryasphlaserthrilleululy-- 127
QY 507 AGGCCCCCATGTCCTCATTACTCGGGTTCATATTTGCTGTTTGTATGATGACATGA 566
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 -----GlnAlaValCyserhegilylephenapolylylegly 140
QY 567 GGAATTCGAGCTCAAAATTTGCTGCAACAGAAATTCATCAAAATTCAGAAATTTT 626
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 Glyseralghalaladlulryleuileuglyuhistreuphenamleuwer---LysHis 159
QY 627 CCTAAGAGAGATGATATCATGTGTAGAAAGACGTGAAGAGATGCTTTTGACACTTC 686
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 ProGln-----Pheleuthrasphthrlylsualaleuansglulhtryr 174
QY 687 AAGCATCTGATGAAAGTTCTTAAACAGCTTCAGCCAGAACCTTCCTGAGAA--- 743
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 Lysglulhtraspvalalaspheleuglu-----serglulysasphthrlyrargasp 191
QY 744 GATGGTTCACCTGCCAGCTGTGTGCTGTGATAGCAACATTTTATATTCCAACCTC 803
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 192 AspgllyserthrlyasexlalaValleuvalgllyashhileuulryalalashval 211
QY 804 GGAAGTATGTCGGCAATCTTGTGTGTATATGAGAGAGTCAAAACATCAGACCTTA 863
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 212 Glyaspserythrilleval-----Serlysaladlylsalalle 225
QY 864 AGCCCTCAGCAAGATATCCATCATCATGATGAGAGCGATGAGATACAGAGGCT 923
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 Alaleuserasphasphlslyspromasrgseraspglularglyasrgllegluserla 245
QY 924 GGAGGAAACGTCAAG-----GATGGCGTGTGTTGGCGGTGCTGATGAGTTCACGC 974
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 Glyglyvalillemetrplaladlythrtrparlyalgllylvalleuallameterarg 265
QY 975 TCCATTTGGGAGAGGAGAGATCAAGCGCTGCGCTGACCTGTGCGCAGATCAGAGCC 1034
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 266 Alaleuulysasphmetleuylseline---ValvalaladlulProbiduliealasp 284
QY 1035 TGCCAGCTGACCCCAATGACAGTTCAATTTTGCTGTGATGAGGCTCTTCAAGTTC 1094
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 Leuglulleasphlsglulaladluleuvalleuallaserasplyleuulrpspal 304
QY 1095 TTTACCCAGAGAGAGAGCGGTGAATTCATCTTGTCTGTCTGAGAGTAAAGATCCAG 1154
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 305 ValProasnglulaspalaval-----AlaleuallaserlulduulPro----- 320
QY 1155 ACCCGGAGAGGAAAGTCCGACCGCACCCCGCTACAGAACAGCTTCGAACAGCTGACC 1214
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 -----GlnAlaAlaAlaarglyserleuthr 328
QY 1215 AACCAAGCGGTGAGCGGGGCTCGGCCGACAACTCATGTGTGTGTGCGGATAGG 1274
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 329 AsphthrlylasersarlglyserlialasphaniethrCyserlvalalysphearg 348
QY 1275 CAC 1277
      |||
Db 349 His 349

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RESULT 17

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081773
ID 081773 PRELIMINARY; PRT; 389 AA.
AC
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 42.6 kDa protein.
GN F28M20.60 OR A14G31750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hohnsels J.,
RA Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.,
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031004; CAI9748.1; -.
DR EMBL; AL161579; CAB7893.1; -.
DR HSSP; P35813; 1A6O.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR000222; P2C.
DR InterPro; IPR001932; P2C-1like.
DR Pfam; PF00481; P2C; 1.
DR SMART; SM00332; P2C; 1.
DR SMART; SM00331; P2C; SIG; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
DR PROSITE; PS01032; P2C; 1.
DR Hypothetical protein.
KW
SQ SEQUENCE 389 AA; 42562 MW; A7C4C39764ECIDEA CRC64;

Alignment Scores:
Pred. No.: 2.05e-22 Length: 389
Score: 368.00 Matches: 114
Percent Similarity: 45.56 Conservative: 40
Best Local Similarity: 33.73 Mismatches: 86
Query Match: 14.37 Indels: 98
DB: 10 Gaps: 14

US-09-935-124A-1 (1-1422) x 081773 (1-389)
QY 426 GGGTATGGCTGAGCGGAAGGAGGAGAGATGCGAGATGCCACGTCATCTG 485
DB 60 G|Y|T|Y|---|A|l|a|s|e|r|P|r|o|g|l|y|a|s|e|r|S|e|r|e|t|u|s|p|h|e|r|y|r|g|l|u|t|h|r|a|g 78
QY 486 AAGCATCATCCAGAGAGTGTAGCCGCCCATCTGCTCCTATTACTCGGTTTCATATTT 545
DB 79 I|e|a|s|p|g|l|v|a|g|l|u|g|l|y|-----|g|l|u|l|e|v|a|l|g|l|e|u|p|h|e 90
QY 546 GCGTCTTTGATGATGATGAGGAATTCAGCTCAAAATTTGCTCCACAGAAATTTGCAT 605
DB 91 G|l|v|a|l|p|h|e|a|s|p|g|l|y|h|s|g|l|y|a|a|a|g|a|a|l|a|g|l|u|t|r|v|a|l|y|s|g|l|a|n|t|e|u|p|h|e 110
QY 606 CAAATTTATGAGGAAATTTCTTAAGGAGATGATTAATCATGTTAGAGAAACCGTGAAG 665
DB 111 S|e|r|a|n|l|e|u|l|e|r|g|---|H|s|P|o|l|y|s|-----|P|h|a|l|e|s|e|r|-----|A|s|p|h|r|t|h|r 124
QY 666 AGATGCTTTTGACACTTTCAGCATCTGATGAGAGATTCTTAACAGCTTCAGC 725
DB 125 A|a|a|l|l|l|e|a|l|a|s|e|r|a|l|a|t|r|y|r|a|n|g|l|n|t|h|r|a|s|e|r|c|l|u|p|h|e|u|l|y|s|e|r|g|l|u|a|n|s|e|r 144
QY 726 CAGAGACGCTGCTGGAAGAT---GGGTCCACTGCGACGCTGTGCTGCTGATAGCAAC 782
DB 726 C|A|G|A|G|A|C|G|T|G|C|T|G|G|A|A|G|A|T|---|G|G|G|T|C|C|A|T|G|C|G|A|C|G|T|G|T|G|C|T|G|A|T|A|G|C|A|A|C 782

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DB 145 G|l|a|n|e|-----|A|r|g|a|s|p|a|l|a|g|l|y|s|e|r|t|h|r|a|l|a|s|e|r|t|h|r|a|l|l|e|u|e|v|a|l|y|a|s|p 161
QY 783 ATTCTTTATATTCGCAACCTCGAGATAGTCCGGCAATCTTGCTGATATATGAGAG 842
DB 162 A|r|g|l|e|u|l|e|v|a|l|a|a|s|e|r|a|l|a|s|e|r|a|l|a|l|l|e|c|y|b|a|r|g|l|y|o|l|y|a|n|---| 180
QY 843 AGTCAAAACATGACGCTTAAGCTTCAGCAAGACATATTCACATGATGAGAG 902
DB 181 -----|A|a|l|l|e|a|l|a|v|a|l|e|r|a|s|e|r|a|s|p|h|i|l|e|y|P|r|o|a|s|p|l|n|s|e|r|a|s|p|l|n 195
QY 903 CGGATGAGGATCAGAGAGCTCGAGAAACGTCAGG-----GATGGCGGTGTTTG 953
DB 196 A|r|g|l|a|a|g|l|l|e|g|l|u|a|s|p|h|i|a|g|l|y|p|h|e|v|a|l|e|r|t|h|r|a|l|g|l|y|t|h|r|t|r|p|r|v|a|l|g|l|y 215
QY 954 GCGTGCCTTAGAGTGTCAAGCTTCATTTGGGAGCGGAGCATGACAGCGCTCGATCAC 1013
DB 216 G|l|y|v|a|l|l|e|u|a|l|v|a|l|e|r|t|h|r|g|a|l|a|h|e|g|l|a|s|p|h|i|l|e|y|a|l|l|e|u|l|y|g|l|n|t|r|---|v|a|l|v|a|l 234
QY 1014 TCTGTGCCCCGACATCAGA----- 1031
DB 235 A|a|a|s|p|r|o|g|l|u|l|l|e|g|l|n|v|a|l|l|e|u|t|h|r|p|h|e|c|y|s|g|l|a|n|t|e|u|l|e|u|t|r|l|e|y|a|n 254
QY 1031 ----- 1031
DB 255 A|a|t|h|r|l|e|u|l|e|u|t|h|r|l|e|g|l|u|h|i|s|a|n|l|e|u|h|i|s|t|r|i|l|e|s|e|r|i|l|e|v|a|l|e|r|t|r|e|u 274
QY 1032 -----CGTGCACGCTGACCCCAATGACAG----- 1058
DB 275 A|e|n|g|l|y|t|h|r|l|e|u|l|a|s|n|p|h|e|u|l|a|r|g|s|e|r|l|e|u|l|e|u|l|e|a|l|a|s|e|r|a|s|p|g|l|y|e|u|t|r|p|a|s|p|v|a|l 294
QY 1059 -----TTCAATTTGTTGGCTGTGATGGCTCTTCAAGTTC 1094
DB 295 G|l|u|y|v|a|l|a|s|p|s|e|r|s|e|r|l|e|u|l|u|p|h|e|u|l|l|e|u|a|l|a|s|e|r|a|s|p|g|l|y|e|u|t|r|p|a|s|p|v|a|l 314
QY 1095 TTACCCCAAGAGAGCCGTGAATTCATCTTGCTGCTGCTGAGAGATGAAAAGATCCAG 1154
DB 315 v|a|l|s|e|r|a|n|g|l|u|a|l|a|v|a|l|g|l|y|e|t|i|l|e|---|l|y|s|a|l|l|e|g|l|u|a|s|p|r|o|----- 330
QY 1155 ACCCGGGAAGGAGAGTCCGACGCGACGCCGCTACGAAGACGCTGCACAGCGTGGCC 1214
DB 331 -----G|l|u|g|l|u|g|l|a|l|a|y|a|n|t|e|u|c 338
QY 1215 AACAGCGCGTGCACGCGGCTCGGCCGACAACTGATGATGGTGGCG 1268
DB 339 M|e|t|G|l|u|a|l|a|t|r|y|G|l|a|a|r|g|l|y|s|e|r|a|l|a|s|p|h|e|n|i|e|t|h|r|c|y|s|v|a|l|v|a|l|y|a|s|p 356
RESULT 18
Q94AT1 PRELIMINARY; PRT; 420 AA.
AC Q94AT1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Pucative phosphatase 2C.
GN AT5G53140.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Tortum M.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamuya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.C., Seki M.,
RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Ecker J.R., Theologis A.,
RT "Full length cDNA of gene MTH8.8/AT5G53140 (GI:9757995).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

```

RP SEQUENCE FROM N.A.
RA Yamada K., Bahi J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onders C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Kaminici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Kallin-Neumann G., Kawal J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shimizu P., Southwick A., Shinzaki K.,
RA Davis R.W., Becker J.R., Theologis A.,
RT "Arabidopsis Open Reading Frame (ORF) Clones."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY045819; AAK76493.1; -
DR InterPro: IPR000222; PP2C-
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C_1.
DR PROSITE: PS01032; PP2C: UNKNOWN 1.
SQ SEQUENCE 420 AA; 45786 MW; C31D84D35159052 CRC64;

Alignment Scores:
Pred. No.: 2.82e-22 Length: 420
Score: 366.50 Matches: 112
Percent Similarity: 50.15% Conservative: 59
Best Local Similarity: 32.84% Mismatches: 109
Query Match: 14.32% Indels: 61
DB: Gaps: 13

US-09-935-124a-1 (1-1422) x Q94AT1 (1-420)

OY 291 ACATCAATATCCAGATGTTAAAGCTGAAGGAAAGGAAAGAAAGAAAGCTCCGAG 350
DB 58 ThSerAlaLyeMetMetValAspThr-----SerAlaGly 69
OY 351 GAAGAGAGAAATGCGAGGAGCTTGGAAGAAAGATTGTAAGCTCTCCGATG 410
DB 70 GluLysArgIleSerLeuValAspMetProGluLysValAspArgIleGlyTyrIle 89
OY 411 ATCTTGGCTGAG-----GGCTATGCTGCTGAGCGGAG 446
DB 90 GlyGlyGlyTyrLysAsnAspArgIleSerLeuSerCysGlyTyrCysSerPheArg--- 108
OY 447 GGTGAAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
DB 109 GlyLysArgSerThrMetGluAspPheTyrAspIleLysAlaSerThrIleGluGly--- 127
OY 507 AGGCCCCATCGCTCCATTAACGCGGTTTCATATTGCTGTTTGAATGAGCATGCA 566
DB 128 -----GlnAlaValCysMetPheGlyIlePheAspGlyIleGly 140
OY 567 GGAATTGAGCTCAAAATTGCTGCAAGAAATTGTCATCAAAACTTAATCAAGAAATTT 626
DB 141 GlySerArgAlaIleGluTyrLeuLysGluIleLeuPheAsnAsnLeuMet---LysHis 159
OY 627 CTTAAAGAGATGTAATCATGAGTGAAGAAACCGTGAAGAGATGCTTTTGAACATTTT 686
DB 160 ProGln-----PheLeuThrAspThrLysLeuAlaLeuAsnGluThrTyr 174
OY 687 AAGCATATGATGAAGAGTCTCTTAACAAGCTTCCAGAGAGCTGCTGGAGAA--- 743
DB 175 LysGluThrAspValAlaPheLeuGlu-----SerGluLysAspThrTyrArgAsp 191
OY 744 GATGGGTGCACTGCAAGCGGTGCTGCTGAGAGAAATTTCTTAATTAATGCAACCTC 803
DB 192 AspGlySerThrAlaSerAlaIleValLeuValGlyAsnHisIleTyrValAlaAsnVal 211
OY 804 GAGATATGTCGGCAATCTGTGCTGTTATTAATGAAGAGAGAGAGAGAGAGAGAG 863
DB 212 GlyAspSerIleThrIleVal-----SerLysAlaGlyLysAlaIle 225
OY 864 AGCTCAGAGAGAGATTAATCAATCAATCAATGAAGAGAGAGAGAGAGAGAGAGCT 923
DB 226 AlaLeuSerAspPheIleLysPheProAsnArgSerAspGluArgIleGluSerAla 245

OY 924 GAGAGAAACCTCAG-----GATGGGCTGTTTGGGCGCTGCTGAGGTGTCAGCC 974
DB 246 GlyIleValIleLeuTyrAlaGlyThrTyrArgValGlyValIleValLeuLysSerArg 265
OY 975 TCCATTGGGAGCGGAGGATGACAGCGCTGCGGTGTCACCTTGCCCAATCAGAGCC 1034
DB 266 AlaPheGlyAsnArgMetLeuLysGlnPhe---ValValAlaGluProGluIleGluAsp 284
OY 1035 TGCCAGCTGACCCCAATGACAGGTTCATTTTGGCTGCTGATGGGCTCTTAAGGTC 1094
DB 285 LeuGluIleAspHisGluLysIleValLeuLeuValLeuLysSerAspIleLysTyrVal 304
OY 1095 TTTACCCCAAGAGAGCGGTGAATTTGCTGCTGCTGCTGAGAGTGAAGATCCAG 1154
DB 305 ValProAsnIleAspAlaVal-----AlaLeuAlaIleSerGluIleGluPro----- 320
OY 1155 ACCCGGAGAGAGAGAGTCCGACCGAGCCGCGCTGACAGAGAGAGAGAGAGAGGTC 1214
DB 321 -----GluAlaIleAlaArgLysLeuThr 328
OY 1215 AACAGCGCTGACAGCGGCGCTGCGCCGACAGCTCATGTATGGTGGCATAGGTC 1274
DB 329 AspThrAlaPheSerArgIleSerAlaAspAsnIleThrCysIleValIleValIleArg 348
OY 1275 CAC 1277
DB 349 His 349

RESULT 19
OQUPRO PRELIMINARY; PRT; 757 AA.
ID OQUPRO;
AC OQUPRO;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE KIA1072 protein.
GN KIA1072.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX NCBI [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=9937452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K., Hirogawa M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 6:197-205 (1999).
DR EMBL: AB028995; BAA83024.1; -
DR HSSP: P35813; 1A6Q.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C SIG. 1.
DR PROSITE: PS01032; PP2C; 1.
SQ SEQUENCE 757 AA; 84177 MW; 45593FC322FCBD3B CRC64;

Alignment Scores:
Pred. No.: 3.43e-22 Length: 757
Score: 366.50 Matches: 123
Percent Similarity: 43.02% Conservative: 68
Best Local Similarity: 27.70% Mismatches: 148
Query Match: 14.32% Indels: 105
DB: Gaps: 18

US-09-935-124a-1 (1-1422) x Q9UPRO (1-757)

OY 123 CCGAGAGCCGAGGCGCTGCGCGCGCGCTGCGGAGAGAGAGAGAGAGAGAGAGCTG 182

Db 87 ProGluProGluGluGlu---AlaAlaValGluGluGluGluGluGluGluGluGluAla 105
Qy 183 CTCTTGTGATGACCTCCCTCCGCGCAGCATGACTGACATGACGAGGAGCTTGTCTT 242
Db 106 ThrAlaAlaAlaAlaProGluHisSerAlaValProPro-----ProProGlu 122
Qy 243 TTTGATGATCTCCACCC-----GCTACAGTGGC 212
Db 123 LeuProProLeuProProLeuProArgProLeuSerGluArgGluLeuVal 142
Qy 273 GATTGAGTTCTCTGTCACATCATATCCAGATGGTAAAGCTGAA----- 320
Db 143 GluGluGluSerLeuSerLeuGluGluGluGluGluGluGluGluGluGluGluGlu 162
Qy 321 ---GGGAAAGAGCAAGAAAGAAAGCTCCGAGAA----- 353
Db 163 LeuAlaAlaAlaLeuAlaArgAlaThrSerArgProGluValLeuGluInSerArgLeuSerAla 182
Qy 354 -----GAGAAAGAAATGGCACTGAAAGACTTGGAAAGAAAGTTTGTAA 398
Db 183 HisGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 202
Qy 399 GCGCTTCGCGTATCTTGGT-----CTGAGGCGCTAT 431
Db 203 LeuAlaArgSerValPheSerGluValHisGluGluLeuGluGluGluGluGluGluGlu 222
Qy 432 GTGGCTGAGCG-----AAGGCTGAG 452
Db 223 ProLeuAlaArgArgProGluInLeuGluGluGluGluGluGluGluGluGluGluGluGlu 242
Qy 453 AGGAGAGAGATGAGAGATGCGCCAGCTGATCTGACGACATCACGAGAGCTGAGGCC 512
Db 243 ArgArgGluMetGluMetGluMetGluMetGluMetGluMetGluMetGluMetGluMetGlu 254
Qy 513 CCATGCTCCCTCATTTCTCGCGT-----TCATATTTTGTGTGTTT 554
Db 255 AspPheAspMetLeuPheAspLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu 274
Qy 555 GATGACATGAGAGAAATTCGAGCCTCAAAATTTGTGACAGAAATTTGTGACAAATTTT 614
Db 275 ArgGluHisGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 294
Qy 615 ATTCAGAAA-----TTTCTTAAAGAGATGTAATGATGTAGAGAAAAGCTGAAAGAG 668
Db 295 ValArgGluGluMetPheProHisArgProAla-----Glu 306
Qy 669 TCGCTTTTGGACCTTGAAGCATGACTGAGATGAGATTCCTTAAAGAGCTTCCAGCCAG 728
Db 307 AlaLeuGluArgAlaPheArgValThrArgGluArgPheValGluValAlaAla----- 324
Qy 729 AAGCCTGCTGGAAGATGGGTCACTGACGACGCTGTCTGCTGTAGACAAATTTT 788
Db 325 ArgGluSerLeuArgGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 344
Qy 789 TATATTCGCAACTCGAAGATAGCTCGGCAATTTGTGCTGTTATATGAGAGAGACTCA 848
Db 345 HisValAlaIleArgValGluArgSerGluValMetLeuValArg----- 358
Qy 849 AAACATGAGCGCTTAAAGCTCAGCAAGAGCATTAATCCAACTAGATGAGAGCGGATG 908
Db 359 LeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 378
Qy 909 AGGATGACAGAGGCTGAGAGAAAGCTC-----AGGATGAGCGGTGTTTGGGCGGTG 959
Db 379 ArgGluGluAlaLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 398
Qy 960 CTAGAGGCTGACGCTCATTTGGGAGCGGAGCATCAAGCGC-----TGGGCTGACCC 1013
Db 399 LeuSerValSerArgAlaIleGluArgAlaGluHisGluGluGluGluGluGluGluGlu 418
Qy 1014 TCTGTGCGCGACATCAGAGCGCTCCAGCTGACCCCAAGAGAGCTCATTTGTTGGCC 1073
Db 419 -----AspSerAlaSerThrValLeuArgGluThrGluMetGluLeuAla 435

Qy 1074 TGTGATGGGCTCTTCAAGGCTTTTACCCCGAAGAGCGGTGAATCTTGTCTCTGT 1133
Db 436 GylArgGluPheThrArgPheThrValAsnProArgGluAlaValGluVal----- 452
Qy 1134 CTGAGAGATGAAAGATCCAGACCCGGAGAGGAAGTCCGCGACCGAGCCCGCTACGA 1193
Db 453 -----SerAspHisLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 467
Qy 1194 GCAGCCTGCAACAGGCTGCGCAACAAAGGCTGACGCGGCGCTCGGCGCAAGCTGACT 1253
Db 468 -----HisGluLeuValAlaSerAlaArgAlaGluGluGluGluGluGluGluGluGluGlu 484
Qy 1254 GTGATGCTGTG 1265
Db 485 ValIleValVal 488
RESULT 20
ID 082469 PRELIMINARY, PRT, 359 AA.
AC 082469;
DT 01-NOV-1998 (TREMBLrel, 08, Created)
DT 01-NOV-1998 (TREMBLrel, 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel, 20, Last annotation update)
DE Protein phosphatase-2C.
GN PP2C.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RX MEDLINE=99200489; PubMed=10102366;
RA Miyazaki S., Koga R., Bohmert H.U., Fukuhara T.;
RT "Issue- and environmental response-specific expression of 10 PP2C
transcripts in Mesembryanthemum crystallinum";
RL Mol. Gen. Genet. 261:307-316(1999).
DR EMBL: AF075580; AAC36698.1; -
DR HSRP: P35813; IACG.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00332; PP2Cc; 1.
DR SMART: SM00331; PP2C_SIG; 1.
DR PROSITE: PS01032; PP2C; 1.
SQ SEQUENCE 359 AA; 39565 MW; 42CCB7092742CD6C CRC64;
Alignment Scores:
Pred. No.: 3,58e-22 Length: 359
Score: 365.00 Matches: 92
Percent Similarity: 52.25% Conservative: 59
Best Local Similarity: 31.83% Mismatches: 94
Query Match: 14.26% Indels: 44
DB: 10 Gaps: 10
US-09-935-124A-1 (1-1422) x 082469 (1-359)
Qy 447 GGTGAGAGGAGAGATGAGATGCGCCAGCTGATCTGAGACATCACGAGAG--- 503
Db 58 GlyProArgGlyTyrMetGluMetGluMetGluMetGluMetGluMetGluMetGluMetGlu 77
Qy 504 -----TGTAGCGCCCATCGCTCCCTCATTTACTCGGGTTTCATATTTGCT 548
Db 78 GylSerLeuPheArgCysProGluProSer-----AlaPheGluGlu 91
Qy 549 GTTTTGTGATGAGATGAGAGATTCGAGCCTCAAAATTTGTGACAGAAATTTGTGACAA 608
Db 92 ValPheArgGluHisGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 111
Qy 609 AACTTAATTCAG-----AAATTTCTTAAAGG-----GATGTATCATGCTGAG 653
Db 419 -----AspSerAlaSerThrValLeuArgGluThrGluMetGluLeuAla 435

Db 112 PhePhePheGluAspValSerPheProGluAlaSerGluLeuAspGluIlePheLeuGlu 131
 Qy 654 AAACCGTAAGAGATGCTTTTGACACTTTCGAACATACCTGAAGAGCTCTTAAA 713
 Db 132 ---GlyValGluAsnCybLeuArgAlaPhePheLeuAlaAsp-----LeuAla 147
 Qy 714 CAAGCTTCCAGCCAGAACCTGCTGGAAAGATGGTCCATGCGCACTGTGTCTGGCT 773
 Db 148 LeuAlaAspAspCysSerIleSerThrSerSerGlyThrThrAlaLeuThrAlaLeuVal 167
 Qy 774 GTAGACACATTTCTTATATTTGCCAACCTGAGATAGTCGGGCAATCTTGTCTGTAT 833
 Db 168 LeuGlyArgLeuLeuLeuValAlaAsnAlaGlyAspCysArgAlaValLeuCybArgLys 187
 Qy 834 AATGAGAGAGTCMAAAACATGCAGCCTTAAGCCTGAGCAAGACATATTCACACTG 893
 Db 188 GlyGlu-----AlaIleAspMetSerGluAspHisArgProThrTyr 201
 Qy 894 TATGAGACCGGATGAGATACAGAGCTGAGAGAAAGTCAGGATGGCGGTGTGTTG 953
 Db 202 ProSerGluLysArgValGluGluLeuGlyLysTyrValAspAspGlyTyrLeuAsn 221
 Qy 954 GGGCTGCTAGAGTGTACAGCTGCAATGGGAGCGGACAGTAAAG----- 998
 Db 222 GlyValLeuSerValSerArgAlaLeuGlyAspTyrAspMetLysLeuProLysGlySer 241
 Qy 999 CGGTGGGCTGACCTCTGTGCGGACATAGACAGCTGCACACTGACCCCAATGACAG 1058
 Db 242 AlaSerProLeuIleSerGluProGluLeuArgGlnIleLeuThrGluAspAspGlu 261
 Qy 1059 TTCAATTTTGTGGCTGTGATGGCTCTTCAAGCTTTTACCCCAAGAAAGCCGTGAC 1118
 Db 262 PheLeuIleIleGlyCysAspGlyIleTyrAspValIleSerSerGlnGlnAlaValSer 281
 Qy 1119 TTCATCTGTCTGTCTGAGAGATGAAAGATCCAGACCCGGAGAGGAGACTCCGACGC 1178
 Db 282 IleVal-----ArgTyrGlyLeuLysArgHis 290
 Qy 1179 GACGCCGCTACGAGCAGCCTGCAAGAGCTGCAACAGACCGCTGACAGCGGCTG 1238
 Db 291 AspAspPro---GluGlnSerAlaLysAspLeuValAsnGluAlaLeuArgHisIleThr 309
 Qy 1239 GCCGACACAGTCACTGTATGATGATG 1265
 Db 310 IleAspAsnLeuThrValIleIleVal 318

RESULT 21
 08WY54 PRELIMINARY; PRT; 766 AA.
 AC 08WY54;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE P22CA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Wu G., Couch F.J.;
 RT Five novel genes from 17q23 amplicon have different amplification and
 RT overexpression frequency in breast cancer."
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF620269; AAF70325.1; -
 DR InterPro; IPR000222; P22C.
 DR InterPro; IPR001932; P22C-like.
 DR Pfam; PF00481; P22C; 1.
 DR SMART; SM00332; P22C; 1.
 DR SMART; PS01032; P22C; 1.
 SO SEQUENCE 766 AA; 85242 MW; E79A909F3F01364B CRC64;

Alignment Scores:

Pred. No.: 4,61e-22 Length: 766
 Score: 365.00 Matches: 122
 Percent Similarity: 42.44% Conservative: 69
 Best Local Similarity: 27.11% Mismatches: 151
 Query Match: 14.26% Indels: 108
 DB: 4 Gaps: 17

US-09-935-124a-1 (1-1422) x 08WY54 (1-766)

Qy 123 CCGAGCCCGGAGCGCTGCGCGCGCGCGCGGAGAAAGACTCAGAAAGCA----- 176
 Db 87 ProGluProGluGluGlu-----AlaAlaValGluGluGluGluGluGluGluAlaAla 105
 Qy 177 -----CCCTGCTCTTGATGAC 194
 Db 106 ThrAlaAlaAlaProGlyHisSerAlaValProProProProGluLeuProPro 125
 Qy 195 CTCCTCCGCGCAGCAGTACTGACTACGATCAGAGGAGAACTTTGCTTTGATGATCTC 254
 Db 126 LeuProProLeuProArgProLeuSerGluArgIleThrProArgProLeuSerGluArg 145
 Qy 225 CCACCCGCTAGCAGTGGCATTCAAGTTCTCTTCCCATCATATCCAGATGGTAAAG 314
 Db 146 IleThrArgGluGluValGluGluGluSerLeuAspLeuProCysLeuGlnGluGluGlu 165
 Qy 315 ACTGA-----CGGAAGACGAAAGGAAAACTCCGAGGA----- 353
 Db 166 TyrAsnCybProSerPheLeuAlaAlaAlaLeuAlaArgAlaThrSerAspGluValLeu 185
 Qy 354 -----GAGAAGATGCGATGAAAGCTTGTG 380
 Db 186 GlnSerAspLeuSerAlaHisTyrIleProLysGluThrSerGlyThrGluGluVal 205
 Qy 381 GAAAGAAAGTTGTAAAGCTCTTGGGTGATCTTGTG----- 419
 Db 206 GlnIleGluThrValLysLeuAlaArgSerValPheSerLysLeuHisGluIleCysCys 225
 Qy 420 -----CTGAAGGCTATGTGCTGACGG----- 443
 Db 226 SerTyrValLysAspPheProLeuArgArgProGluLeuTyrTyrGluThrSerIle 245
 Qy 444 -----AAGGTGAGAGGAGGAGATGAGAGATCCACGCTCATCTGAAACGATC 494
 Db 246 HisAlaIleLysAsnMetArgArgLysMetGluAspLysHisVal----- 260
 Qy 495 ACCGAGAGTGTAGCGCCCATCGCCCTCATCTCGGCT----- 536
 Db 261 -----CysIleProAspPheAsnMetLeuPheAsnLeuGluAspGlnGluGluGln 277
 Qy 537 TCATATTTGCTGCTTTTATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 596
 Db 278 AlaTyrPheAlaValPheAspValHisIleValAlaSerAlaIleTyrAlaSerIle 297
 Qy 597 AATTGCAACAAACTTAATCAGAAA-----TTTCTTAAAGAGATGTAAATCAGTGA 650
 Db 298 HisLeuHisValAsnLeuValArgGlnGluMetPheProHisAspProAla----- 314
 Qy 651 GAGAAACCGTGAAGAGATCTTTTGACACTTTCAGACATTCGATGAAGAGTCTT 710
 Db 315 -----GluAlaLeuCybArgAlaPheArgValThrAspGluArgPheVal 329
 Qy 711 AAACAGCTTCCAGCCAGAACGCTCGAAGAGTGGTCACTGCCAGTGTCTG 770
 Db 330 GlnLysAlaAla-----ArgIleSerLeuArgCysGlyThrThrGlyValValThrPhe 347
 Qy 771 GCTGTAGACAAATCTTATATTTGCCAACTCCGAGATAGTGGGCAATCTTGTGTGCT 830
 Db 348 IleArgGlyAsnMetLeuHisValAlaIleTyrValGlyAspSerGlnValMetLeuValArg 367
 Qy 831 TATATAGAGAGAGTCAAAACATGACACCTTAAGCTCAGCAAGAGCATATCAACT 890
 Db 368 -----LysGlyGlnAlaValGluGluMetLysSerProHisIleLysProAsp 381

QY	891	CAGTATGAAGACCGAGTACAGATTCACAAAGGCTGAGAAAGCTC-----AGGAT	941
DB	362	ArgGuaArgGlnUlybGlnAlaGlyLeuAlaLeuAlaGlyCysAlaValAlaTrpHeGlyAla	401
QY	942	GGGCGCTGTTTGGCGCGCTGCTAGAGGTGTCAAGCTTCATTTGGGGACGGGACATACAGCGC	1001
DB	402	TrpArgValaGlnGlySerLeuSerValSerArgAlaIleGlyYAspAlaGlnIleYAspPro	421
QY	1002	-----TGGGTGTCACTCTGTGTGCCCCGACATCAAGACGCTGCACGCTGACCCCCAATAC	1055
DB	422	TyrIleCysGlyYAspAla-----AspSerAlaSerThrValLeuYAspGlyThrGlu	438
QY	1056	AGGTTCATTTTGGCGCGCTGATGAGGCTCTCAAGGCTTTTACCACAGAAAGCGCG	1115
DB	439	AspTyrLeuIleLeuAlaCysAspGlyPheTyrAspThrValaAsnProAspGluAlaVal	458
QY	1116	AACCTCATCTTGTCTCTGTCTCGAAGATGAAMAATCCAGACCCGGAGAGGAACTGCCA	1175
DB	459	LySValVal-----SerArgHisLeuIleGlyIleuYAsnAsnIlyAspSerSer	473
QY	1176	GCCAGACGCCCTACGAAGACCTGCACAAAGCTGGCCAAAGCGGCTGACGGGGC	1235
DB	474	MetValAla-----HisIlyLeuValAlaSerAlaArgAspAlaGly	487
QY	1236	TGGCGGACAAAGTCACGTGTATGATGTTGGTG	1265
DB	488	SerSerAspAsnIleThrValIleValVal	497
RESULT 22			
Q9LEW5		PRELIMINARY;	PRT; 348 AA.
AC	Q9LEW5		
DT	01-OCT-2000	(TREMBLrel.15, Created)	
DT	01-OCT-2000	(TREMBLrel.15, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel.20, Last annotation update)	
DE	Protein phosphatase 2C-like protein.		
GN	T30N20.10.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eustrodes II; Brassicales; Brassicaceae; Arabidops.		
OX	NCBI_TaxID=3702;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RA	Beyan M., Pereira S.A., van Staveren M., Dirkse W., Stiekema W.,		
RA	Barcoff I., Meeres H.W., Ruid S., Lemcke K., Mayer K.F.X.;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
RN	(2)		
RA	SEQUENCE FROM N.A.		
RA	EU Arabidopsis sequencing project;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL365234; CAB96829.1;	-	
DR	HSSP; P35813; 1A6O.		
DR	InterPro; IPR001993; Mitoch.carrier.		
DR	InterPro; IPR000222; PP2C.		
DR	InterPro; IPR001932; PP2C-like.		
DR	Pfam; PF00481; PP2C.1.		
DR	SMART; SM00332; PP2C_S1G.1.		
DR	SMART; SM00331; PP2C_S1G.1.		
DR	PROSITE; PS00215; MITOCH.CARRIER; UNKNOWN_1.		
DR	PROSITE; PS01032; PP2C.1.		
QO	SEQUENCE	348 AA; 37379 MW; 12447BB07F740E2C CRC64;	

Alignment Scores:	
Pred. No.:	
Score:	3,99-22
Percent Similarity:	364/50
Best Local Similarity:	53.00%
Query Match:	36.40%
DB:	14.24%
	10
US-09-935-124A-1 (1-1422) x Q9LEW5 (1-348)	
Length:	348
Matches:	103
Conservative:	47
Mismatches:	86
Indels:	17
Gaps:	13

Oy	426	GGCTATGTGGCTGAGCGGAGGCGGTGAGAGGAGAGATGCAGAGT---	GCCACGCTATC	482
Db	35	GIlyTyr---AlaSerSerAlaGIlyLysArGSerSerMetGluAspPhe	pheGluThrArg	53
Oy	483	CTGAACAACATCAACCGAGAGGTGTAAGGCCCCCATCGTCCCTATTACTCGGGTTTCATAT	542	
Db	54	IleAerGlyIleAerGlyGluIle-----	ValGlyIleu	64
Oy	543	TTTGCTGTTTTGATGACATGAGAGAAATTGAGCTCAAAATTGCTGCACAGAAATTG	602	
Db	65	PheGlyValPheAerGlyHisGIlyAlaArgAlaAlaGIlyTyrValLysArgHisIleu	84	
Oy	603	CATCAAAACTTAATCAGAAAAATTTCTTAAGAAGATGTAATGAGTGTAGAAAAACGTG	662	
Db	85	PheSerAsnIleuIle---ThrHisProLys-----PheIleSer-----	AspThr	98
Oy	663	AAGAGATAGCCTTTTGAGCATCTTCAAGCACTTACTGATGAGAGATGTTCTTAAACAAGCTTCC	722	
Db	99	LysSerAlaIleThrAerAlaTyrAlaAsnValGIlyAspSerAerAlaValIleSerArgGIlyLys	118	
Oy	723	AGCCAGAAGCCTGCGTGGAAAGAT---GGGTCACTGCGCACGTGTGTTCTGGCTGTAGAC	779	
Db	119	SerHisAsn-----ArgAerAlaGIlySerThrAlaSerThrAlaIleuValGIly	135	
Oy	780	AACATCTCTTAATATATGCGCACTCTCGAGATATAGTCGGGCAATCTTGTCGTATATATAG	839	
Db	136	AspArgLeuValValAlaAsnValGIlyAspSerAerAlaValIleSerArgGIlyLys	155	
Oy	840	GAGAGTCAAAAACATGACGCTTAACCTCAGCAAGACATAAATCCAACTCAGTATGAA	899	
Db	156	-----AlaIleAlaValSerAerAerHisLysProAspGlnSerAsp	169	
Oy	900	GAGCGATGAGGATACAGAAAGCTGAGAGAAACGTCAAGGATGGCGTGTGGCGCTG	959	
Db	170	GIuArgGIuArgIleGIuAsnAlaGIlyGIlyPheVal-----MetTrpAlaGIlyAl	186	
Oy	960	CTAAGAGTGCACGCTCCATTTGGGAGCGGAGCATCAACGCTGGCGGTGACCTCTGTG	1019	
Db	187	LeuAlaValSerAerAlaPheGIlyAspAerGlyLeuLysGlnTyr--ValValAlaAsp	205	
Oy	1020	CCGACATCAAGACGCTGCCAGCTGACCCCCCAATGACAGGTTTCATTTGTGGCTGTGAT	1079	
Db	206	ProGluIleGlnGluGlyLysIleAerAspThrLeuGluPheLeuIleuAlaSerAsp	225	
Oy	1080	GAGGCTCTTCAAGGCTTTTATCCCAAGAAAGACCGGTGACTTATCTGTCTCGAG	1139	
Db	226	GlyLeuTrpAerValPheSerAsnGIuAlaAlaValAlaMetVal-----	240	
Oy	1140	GATGAAAAAAGATCCAGACCGCGAAAGGAATGCCGACCGCACCGCGGTAGGAAGACCC	1199	
Db	241	-----LysGIuValGIuAspPro-----GluAspSer	249	
Oy	1200	TGCACAAGCTGCGCAACAGCGGTCGACGCGGCTCGGCGCAACAAGTCACTGTGATG	1259	
Db	250	AlaLysLysLeuValGIlyGlyAlaIleLysArgGlySerAlaAspAsnIleThrCysVal	269	
Oy	1260	GTGTGTCGG	1268	
Db	270	ValValArg	272	
RESULT 23				
O9FXE4	1D	PRELIMINARY; PRT; 464 AA.		
AC	O9FXE4			
DT	01-MAR-2001	(T-EMBLrel. 16, Created)		
DT	01-MAR-2001	(T-EMBLrel. 16, Last sequence update)		
DT	01-MAR-2002	(T-EMBLrel. 20, Last annotation update)		
DE	Fl1A21.5			
OC	Arabidopsis thaliana (Mouse-ear cress).			
OC	Burkholderia viridiplantae, Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			

RESULT 23

Q9FXE4	PRELIMINARY;	PRT;	464 AA.
ID	Q9FXE4		
AC	Q9FXE4;		
DT	01-MAR-2001 (T-EMBLrel. 16, Created)		
DT	01-MAR-2001 (T-EMBLrel. 16, Last sequence update)		
DT	01-MAR-2002 (T-EMBLrel. 20, Last annotation update)		
DE	Fl1A21.5.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eudots II; Brassicales; Brassicaceae; Arabidopsids.		
OX	NCBI Taxid=3702;		


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OX NCBI_TaxID=3702;
RN
SEQUENCE FROM N.A.
RA Yamada K., Barni J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.U., Tang C., Tortum M., Yamamura Y., Y.G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones B., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koeseima E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shimizu P.,
RA Southwick A., Tracy S.E., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL "Full Length cDNA of gene T20B5.6/At2g40860 (GI:2623300).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AY056151; AAL07230.1; -
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR001932; P2C-like.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00481; P2C; 1.
DR Prodom: PD000001; Euk_Pkinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
KM ATP-binding: Hypothetical protein; Transference.
SQ SEQUENCE 658 AA; 72852 MW; 66041EE6EAEFE14 CMC64;

Alignment Scores:
Pred. No.: 1,05e-21 Length: 658
Score: 360.50 Matches: 127
Percent Similarity: 41.82% Conservative: 57
Best Local Similarity: 28.86% Mismatches: 137
Query Match: 14.08% Indels: 119
DB: 10 Gaps: 17

US-09-935-124a-1 (1-1422) x Q940A2 (1-658)
QY 84 CTCAC---CGACCTCCGCCATGACCTCTCGGGACCTCCGAGCCCGACGCTCG 140
DB 280 LennileuProllyserleuSerleuileGlnaCysTrpGluSerAspProSer 299
QY 141 CCGCGCCGCGCTGCC----- 155
DB 300 LysArgProSerSerAspAsnValValleuGluLeuGluSerIleTrpGluGlnValArg 319
QY 156 GGGAGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 215
DB 320 GlyLys-----GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 337
QY 216 GACTCAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 275
DB 338 Asp-----GlyAlaAspIleIle-----LysAsnSerGlyAsp 348
QY 276 TCAAGTTCTCTCCACCATATATCCAGATGTAAAGATGAGAGAGAGAGAGAGAG 335
DB 349 TyrArgAspThrValAsnTrpPheSerGln-----GlyGluCysLeuSer 363
QY 336 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 395
DB 364 LysLysSerSer----- 367
QY 396 AAGAGCTCTTCGATCTCTTCGATCTTCGATCTTCGATCTTCGATCTTCGATCTTC 446
DB 368 -----ValSerThrValPheAspValLysLeuTrpSerSerSerThrAspGluProSer 385
QY 447 -----GTTGAAGAGAGAGAGATG 464
DB 386 ArgTyrValProValIleSerCysGlySerPheAlaThrCysGlyArgArgGluSerMet 405
QY 465 CAGATGCCAGATCTCTTCGATCTTCGATCTTCGATCTTCGATCTTCGATCTTCGAT 524
DB 406 GluAspThrIlePheIleIleProIleMetCysAsnGln----- 418
QY 525 ATTAAGCTGATTCATATTGCTGTTTGTATGATGATGATGATGATGATGATGATGAT 584
::: |||||:::||||||| |||

DB 419 ---GluSerIleIleHisLeuPheAlaIlePheAspGlyHisArgGlyAlaAlaAlaGlu 437
QY 585 TTTCGTCACAGAGATTTTCGATCAAAATTAATCAAGAAATTTCTTAAGAGATTAATC 644
DB 438 PheSerIleGlnValLeu-----ProGlyLeuValGln 448
QY 645 AGTGTAGAGAAAC---GTGAGAGATGCTTTTGGACATTTCAAGCATATCTATGAA 701
DB 449 SerLeuCysSerThrIleArgIleGluValLeuSerGlnAlaPheValArgThrAspLeu 468
QY 702 GAGTTCTTAACAGAGCTTCACCGCAGAGAGCTTCC-----TGG 740
DB 469 AlaPheArgGlnIleuLeuAspSerHisArgGlnSerIleValSerGlnLysAspTrp 488
QY 741 AAGATGAGTTCACCTCCACGATGTTCTGCTGATGACACATTTCTTAATATTCACAC 800
DB 489 HisProGlyCysThrAlaIleAlaSerLeuLeuValGlnLeuLysLeuPheValAlaAsn 508
QY 801 CTCGAGATATGTCGGGCAATCTTGTCGTATATAGAGAGAGATCAAAAATCATCAACC 860
DB 509 ValGlyAspSerArgIleIleLeuCysArgIleGlyHis-----Pro 522
QY 861 TTAGCCTCAGAGAGAGATATCACTCACTCACTCACTCACTCACTCACTCACTCACT 920
DB 523 PheAlaLeuSerIleValHisLeuAlaThrCysIleAspGluArgAsnArgValIleGly 542
QY 921 GCTGAGAGAAAGCTCAG-----GATGGCGTGTCTTGGCGCTG---CTAGAG 965
DB 543 GluGlyValArgIleGluTrpLeuValAspThrTrpArgValAlaProAlaGlyLeuGln 562
QY 966 GTGTACGCTTCCTTTGGGAGACGGGAGATACAGCGCTCGGCTTCCTCTGTGGCGGAC 1025
DB 563 ValThrArgSerIleIleGlyAspAspLeuLysPro---AlaValThrAlaGluProGlu 581
QY 1026 ATCAGACGCTGCGACGTGACCCCAATGACAGTTCAATTTGTCGCTGTGATGGCTC 1085
DB 582 IleSerGluThrIleLeuSerAlaAspAspGluPheLeuValMetAlaSerAspGlyLeu 601
QY 1086 TTCAAGTCTTTATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1145
DB 602 TrpAspValMetAsnAspGluGlnValIleGlyIleIleArgAspThrValLysGluPro 621
QY 1146 AAGATCCAGACCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205
DB 622 SerMetCysSerLys----- 626
QY 1206 AGGCTGGCCAAAGAGCGGTGACGCGGGGCTCGGCCGACACGTCATGTGATGGTGTG 1265
DB 627 ArgLeuAlaThrGlnAlaAlaAlaArgGlySerGlyAspAsnIleThrValIleValVal 646

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Search completed: February 9, 2003, 18:00:30
Job time : 123 secs

KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX Homo sapiens.
OS
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 05-DEC-2000; 2000US-0251988.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.

PR 05-JAN-2001; 2001JUS-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI: 2001-465566/50.
DR N-PSDB: AAS41436.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT palmarmary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases -
XX Claim 11; SEQ ID No 1562; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AA040785-AA03164) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy. AA0229515-AA03814 represent the novel human enzyme polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at wipo.int/pub/published_pat_sequences.

SQ Sequence 441 AA;

Alignment Scores:

Pred. No.:	4,72e-18	Length:	441
Score:	2199.00	Matches:	422
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.90%	Indels:	0
DB:	22	Gaps:	0

US-09-935-124A-1 (1-1422) x AAU23566 (1-441)

[illegible]

Dd	139	GIUGIULeuValGIuIuIyIuIyValIcYeuIaIaIeSerValIIlePheGIuIeuIySeGI	158
Qy	429	TATGGCTGAGCGGAAGGGGTGAGAGAGAGAGATGACAGATGCGCAAGCTTCCGTAC	488
Dd	159	TyValAIaGIuIuIyIuIySeGIuIuIaIaGIuIuIuIeGIuIuIeGIuIuIaIaIeIuIuIe	178
Qy	489	GAACTTACCGAGAGATGTAAAGCCCCCATGTGCCATTAATCTGGGGTTCAATATTTCCT	548
Dd	179	ASpIaIeIuIuIeGIuIuIcYbAaGrProPSeSerSeIuIleIuIaIaIaIeIyIuIeIuIa	198
Qy	549	GTTTTTGAATGACATGAGGAAATTGAGGCTCAAAATTGGCTGACAGAAATTGCATCAA	608
Dd	199	ValPheASpGIuIuIaSeGIyGIuIleIaIaIaIaIeIuIyPheAIaIaIaGIuIuIeIuIaIa	218
Qy	609	AACTTAATACAGAAATTTCTTAAAGAGATGTAACTCACTGTAAAGAAAACCGTAGAGCA	668
Dd	219	ASuIeIuIleIaIuIyIuIyPheProIySeGIuIaIaIeSerValIIeSerValGIuIyIuIyIaIa	238
Qy	669	TGCGTTTGGACACTTTCACGACATACCTGTATGAGAAATTCCTTAAACAAGCTTCCAGCG	728
Dd	239	CyLeuIeIuIaASpIuIuIyPheIySeIuIaIaIaIaIaIeGIuIuIeIuIySeGIuIaIaIeSeGIuI	258
Qy	729	AAACCTGCTGGAAGAAATGGGCTCACTGGCAAGTGTGTCTGGCTGTAGACAACATTCCT	788
Dd	259	IyPheProAIaIuIyIuIyASpGIySeIuIuIaIaIaIeIuIySeValIeIuIaIaIaIePheIIeIu	278
Qy	789	TATATGCGCAACTCGGAGATAGTCCGGCAATCTGTGTCTTATATAGAGAGAGTCAA	848
Dd	279	Ty-IIeIaIaIeIuIeGIuIyASpSeIuIaIaIeIuIeIuIeIuIyIaIaIeIuIyIaIaIeIuIe	298
Qy	849	AAACATGACGACCTTAAGCTCAGCAAAAGACATATCCAACTCAGATGAGAGAGCGAGT	908
Dd	299	IyHIIeIaIaIaIeIuIeSeIeIuIeSeIuIySeGIuIuIaIaIaIeProIuIuIuIyIuIuIuIe	318
Qy	909	AGGATTCAGAAAGCGTGAAGAAACGTCAAGATATGGCGGTGTTGGCGCGTCCAGAGTG	968
Dd	319	ATeIIeGIuIyIaIaIeGIyGIuIyIaIaIaIaIaIaIaIaIaIaIeGIuIaIaIeGIuIaIa	338
Qy	969	TCAAGCTCATATGGGAGACGGGCAAGTCAAGCGCTCGGATGCACCTCTGTGCCCGCAATC	1028
Dd	339	SeIaIySeIeIIeGIyIaIaIeGIuIyIuIyIaIaIaIaIaIaIaIaIaIaIeIuIaIaIeIuIa	358
Qy	1029	AGAGCTGTCACAGTCAACCCCAATGACAGGTTCAATTTGTGTGCTGTGATGGGCTCTTC	1088
Dd	359	ATATATGCTGAGIuIeIuIuIaIaIaIaIaIaIaIaIaIaIeIuIaIaIaIaIaIaIaIaIeIuIa	378
Qy	1089	AAAGTCTTTATACCCCAAGAAAGCCGTGAATCTTGCATCTTGTCTGTCTCGAGATGAAGA	1148
Dd	379	IyValAIaIaIeIuIuIyProGIuIuIuIaIaIaIaIaIaIaIeIuIeIuIaIaIaIaIaIaIaIaIa	398
Qy	1149	ATCAACAACCCCGGAGAAAGGAAGTCCGAGCGGACAGCGCCGCTTACGAAGCAGCGTCCAA	1208
Dd	399	IIeGIuIuIa	418
Qy	1209	CTGAGCGCAACAAGCGGTGACAGCGGGCTCGGCGCAACGTCACTGATGATGGTGGCG	1268
Dd	419	IeIuIaIaIeIuIyIa	438
Qy	1269	ATAGAGGAC 1277	
Dd	439	IIeGIyHIS 441	
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AAU22933			
ID	AAU22933	standard; Protein; 446 AA.	
XX	AAU22933;		
XX	17-DEC-2001	(first entry)	
XX	Novel human enzyme polypeptide #19.		
XX			

KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW 11ase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW neoplastic; anticoagulant.
XX
OS Homo sapiens.
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
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PR 07-JUN-2000; 2000US-0209467.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249247.
PR 17-NOV-2000; 2000US-0249255.
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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251858.

DT	11-JAN-2002 (first entry)	
DE	Human protein phosphatase 2C homologue, SEQ ID NO:2687.	
XX		
XX		
KM	Human; cytokine; cell proliferation; cell differentiation; growth factor;	
KM	haematopoiesis regulation; tissue growth; immunomodulator; activin;	
KM	inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;	
KM	proliferation; metastasis; cancer; tumour; haematopoietic disorder;	
KM	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;	
KM	chronic inflammatory condition; proliferative retinopathy;	
KM	atherosclerosis; coronary heart disease; arterial ischaemia;	
KM	bone disorder; osteoporosis; vascular growth disorder;	
KM	tissue regeneration; wound healing; infection; immune disorder;	
KM	cell culture; drug screening; gene therapy; antiinflammatory;	
KM	antiaesthetic; antiarthritic; haemostatic; antiatherosclerotic;	
KM	cytostatic; osteoparathic; vasotropic; cardiant; virucide; antibacterial;	
XX	antifungal; vulnerary; antilucer.	
OS		
XX	Homo sapiens.	
PN	WO200157188-A2.	
XX		
PD	09-AUG-2001.	
XX		
PF	05-FEB-2001; 2001WO-US03800.	
XX		
PR	03-FEB-2000; 2000US-0496914.	
PR	27-APR-2000; 2000US-0560875.	
XX		
PA	(HASE-) HASEQ INC.	
XX		
PI	Tang YT, Liu C, Drmanac RT;	
DR	WPI; 2001-457740/49.	
XX		
XX	N-PSDB; ABA09561.	
PT		
PT	Human proteins and DNA encoding sequences useful for preventing,	
PT	treating or ameliorating a medical condition in a mammalian subject	
PT	e.g. arthritis and cancer -	
PS	Claim 20; Page 330; 1963pp; English.	
XX		
CC	Sequences ABB10981-ABB1230 represent 1350 novel human polypeptides, and	
CC	sequences ABA08225-ABA09574 represent nucleic acids encoding them. The	
CC	invention also relates to vectors and recombinant host cells comprising a	
CC	nucleotide of the invention, methods of producing the novel polypeptides,	
CC	antibodies against the polypeptides, methods of detecting the nucleotides	
CC	or polypeptides in a sample, and methods of identifying compounds which	
CC	bind to polypeptides of the invention. Although novel, many of the	
CC	polypeptides of the invention have homology to known proteins, thereby	
CC	giving an insight into their probable biological activities, and hence	
CC	potential therapeutic applications. The polypeptides of the invention may	
CC	have various activities, including cytokine, cell proliferation or cell	
CC	differentiation activities; stem cell growth factor activity;	
CC	haematopoietic regulatory activity; tissue growth factor activity;	
CC	immunomodulatory activity; activin- or inhibin-related activities;	
CC	chemotactic or chemokinetic activities; haemostatic, thrombotic or	
CC	thrombolytic activities; receptor or ligand activities; or may be	
CC	involved in oncogenesis, cancer cell proliferation or metastasis.	
CC	Depending on their biological activities, polypeptides and nucleotides of	
CC	the invention are useful for preventing, treating or ameliorating medical	
CC	conditions, e.g., by protein or gene therapy. Such conditions include	
CC	cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell	
CC	disorders), chronic inflammatory conditions (e.g., asthma or arthritis),	
CC	proliferative retinopathy, atherosclerosis, coronary heart disease,	
CC	arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal	
CC	vascular growth. Polypeptides involved with tissue regeneration and	
CC	repair (or nucleic acids encoding them) may be used to promote wound	
CC	healing (e.g., of burns, incisions and ulcers), while those with	
CC	immunomodulatory activities may be used in the treatment of viral,	
CC	bacterial and fungal infections in addition to immune disorders.	
CC	Polypeptides with growth factor activity may be used in cell cultures to	
CC	promote cell growth. For example, such polypeptides may be used to	

Db	268	Ala111eLeuCYaArgTyAaenGluSerGlnTyH1aLa1a1aLeuSerLeuSerTy	287
Qy	876	GACATATATCAACCTCACTATATGAAGACGGATATGAGATATCAAGAGCGTCGAGAAACGTC	935
Db	288	GLuH1aAsnProThGlnTyGluGluWagMetArg11eGlnTySa1aG1yG1yAenVal	307
Qy	936	AGGATAGGGCCGCTTTTGGGGGCGCTAAGATGTCACCGCTCAATGGGGACGGGCGATC	995
Db	308	AlaAspG1yAlaValLeuG1yValLeuG1yValLeuG1yValSerArgSer11eG1yAspG1yGlnTy	327
Qy	996	AAACGCTGGGTGTCACTCTGTGCCGACATCAAGCGTGCAGCTGACCCCAATGAC	1055E
Db	328	LYaYSYCYG1yValThSerValProAsp11aArgArgCYG1yGlnLeuThrProAsnAsp	347
Qy	1056	AGGTCATTTTGTGTGGCTGTGATGGGCTTTCAAGTCTTTCACCGTCTTACCCCAAGAAAGCCGTG	1115E
Db	348	AlaPhe11aLeuLeu1a1aCYaAspG1yLeuPheTySValPheThrProGluGlu1a1aVal	367
Qy	1116	AACTCATCTGTCTCTGTCTCTGAGAGATGAAGAAAGATCCAGACCCGGAGAAAGGATCGCA	1175T
Db	368	AsnPhe11aLeuSerCYeLeuGluAspG1yVal11eGlnThrArgGluG1yTySera1a	387
Qy	1176	GCGCAGACCCCGTATCAAGACAGCGCTGCGCAACAGCGTGGCCCAACAGGCGGTGACGCGGCG	1233E
Db	388	AlaAspAlaArgTyGluAla1a1aCYaAsnArgLeu1a1aenTySa1aValaGlnArgG1y	407
Qy	1236	TCGCGCAGACAGTCATCATGTATGATGGTGGTCCGATATGGGCGAC	1277
Db	408	Ser11aAspAsnValThValMetValValAlaArg11eG1yH1a	421
RESULT 4			
ID	AAAM0555	AAAM0555	
XX	AAAM0555	standard: Protein: 421 AA.	
XX	AAAM0555;		
DT	22-OCT-2001	(first entry)	
DE	Human polypeptide SEQ ID NO 5486.		
XX	Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemocarcin;		
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;		
KW	leukaemia.		
OS	Homo sapiens.		
XX	XX		
PN	WO200153312-A1.		
XX	26-JUL-2001.		
XX	XX		
PF	26-DEC-2000; 2000MO-US34263.		
PR	21-JAN-2000; 2000US-0488725.		
PR	25-APR-2000; 2000US-0552317.		
PR	09-JUL-2000; 2000US-0538042.		
PR	19-JUL-2000; 2000US-0620312.		
PR	13-AUG-2000; 2000US-0653450.		
PR	14-SEP-2000; 2000US-0662191.		
PR	19-OCT-2000; 2000US-0653026.		
PR	23-NOV-2000; 2000US-0727344.		
XX	XX		
PA	(HYSB-) HYSBQ INC.		
XX	XX		
F1	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,		
F1	Wang J, Zhang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;		
F1	Zhao QA, Zhou P, Goodrich R, Drmanac RT;		
XX	XX		
XX	WPI; 2001-442253/47.		
XX	N-PSDB; AA159711.		

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

Example 2; SEQ ID NO 5486; 10078bp; English.

The invention relates to human nucleic acids (AA157798-AA151359) and the encoded polypeptides (AA153642-AA42213) with neurotropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemia and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

SQ Sequence 421 AA;

Alignment Scores:	
Pred. No.:	2,848-212
Score:	213.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	83.71%
DB:	22
Length:	422
Matches:	413
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
DB:	0

US-09-935-124A-1 (1-1422) X AAM40555 (1-421)

[illegible]

```
QY 636 GATGTAATCAGTGTAGAGAAAACCGTAGAGAGATGCCCTTTGGACACTTTCAAGCACTACT 695
XX |||||||
DB 208 AAGVAILLESERVALGIVLSTHRTVALYARGCYLEULEUMAPHRPHELYSHLESTR 227
QY 696 GATGAGAGATCTCTTAAACAAGCTTCACGCCAAGACCTGCCGAAAGAATGGGTCACT 755
XX |||||||
DB 228 AAGGIVGIVPHELEULEUYEGVINALASERSEGINLYSPROVALATRYAPBGILYSERSTR 247
QY 756 GCCACGTGTCTTGGCTGTAGACAACATCTTATATATGSCCAACCTCGAGATAGTCCG 815
DB 248 AATHTCYVALLEULALVALAAPHENILLEUTYRILLEALASNLEUGLYAPSERSTR 267
QY 816 GCATGTTGTGCTGTATATAAGAGAGAGTCAAAAATGACAGCTTTAAGCCTTACAGCAA 875
DB 268 AATLEULEUCYARGTYRANGIVGIVSERGINLYSHILEALALEUSERLEUSERLYS 287
QY 876 GAGCATATATCCATCAGATATGAAAGCCGATAGATATACAGAAAGCTGAGAGAAACCTC 935
DB 288 GIVHIAAPNPTOTHRTGINTYRGIVLARGMETARGILLEGINLYSHIAGLYIYAPENVAL 307
QY 936 AGGAGATGGCGCTGTTTGGCGCTGTAGAGAGTGTACAGCTCCATTGGGAGCGGACAGTAC 995
DB 308 ARGAPBGILYARGVALLEUGLYVALLEUGLYVALSERHTRSERILLELYAPBGILYGINTYR 327
QY 996 AAGCGCTGGCGGTGTCACTCTGTGCCCGACATGACAGCTGCCAGCTGACCCCAATGAC 1055
DB 328 LYVARGCYEGLYVALTHRSERVALPROAPRILEARGARGCYEGVINLEUTHRPROAPNAPR 347
QY 1056 AGGTATATTTTGTGGCTGTGTATGGGCTTTTGAAGTCTTTTACCCCAAGAAAGCCGTG 1115
DB 348 ARGPHIILEULEULALCYAPAPBGILYLEUPHELYVALPHERTHRPROGIVGIVLALVAL 367
QY 1116 AACTTCATCTTGTCTGTCTCGAGATGAAAGATCCAGACCGGAGAGAGAGTCCGCA 1175
DB 368 AAPHPHIILEUSERCYSEULEUGLYAPBGILYSHILEGINTHRTGIVGIVLYSSERIAL 387
QY 1176 GCCGACGCGCGCTAGCAAGACGCTTGCAACAGGCTGGCCAAAGGCGGTGACGCGGAC 1235
DB 388 AIAAPRALIARGTYRGIVLAIALACYSAPNARGLEUALIAPNLYSVALVALGINARGGIV 407
QY 1236 TGGCGCGACAACTCACTGTGATGGTGTGCGGATAGGCGAC 1277
DB 408 SERIALAPAPNVALTHRTVALMETVALVALARGILLEGLYHIS 421
RESULT 5
AAB28791
ID AAB28791 standard; Protein; 392 AA.
XX
AC AAB28791;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human hydrolase-like molecule 2 protein.
XX
KW Hydrolase-like molecule; human; cell proliferation disorder;
KW autoimmune; cancer; AIDS; acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN US6132964-A.
XX
PD 17-OCT-2000.
XX
PF 06-FEB-1998; 98US-0013881.
XX
PR 06-FEB-1998; 98US-0013881.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman, O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;
XX
DR WPI; 2001-006133/01.
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DR N-PSDB; AAC60224.
XX
PT New human hydrolase-like molecules (HNLs) and polynucleotides encoding
PT the HNLs, useful for diagnosing, treating or preventing cell
PT proliferation (e.g. bone cancer) or autoimmune disorders (e.g. AIDS or
PT asthma)
XX
PS Claim 1; Column 43-46; 38pp; English.
XX
CC The present invention relates to isolated and purified cDNA encoding a
CC human hydrolase-like molecule (HNL), designated HNL-1 to HNL-8. The
CC HNLs DNAs and polypeptides are useful for diagnosing, treating or
CC preventing cell proliferation disorders and autoimmune disorders. Cell
CC proliferation disorders include cancers, autoimmune disorders include
CC AIDS (acquired immune deficiency syndrome). The present sequence
CC is a HNL protein of the invention.
XX
SQ Sequence 392 AA;
XX
Alignment Scores:
Pred. No.: 2,31e-199 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: DB: Gaps: 0
US-09-935-124A-1 (1-142) x AAB28791 (1-392)
QY 102 ATGACATCTTGTGGGAGACTGCGGAGCCGAGCGCTGCGCGCGCTCCCGGAGAA 161
DB 1 METAPLEPHEGILYAPLEUPROGIVARGSERPROALALAGLYYS 20
QY 162 GAAGCTCAGAAAGACCCCTGCTTTGATGACTCCCTCCGCGGACAGTACTGACTCA 221
DB 21 GIVLAIAGIVLVSGLYPROLEUPHEAPNAPLEUPROFOLASERSETHRSPER 40
QY 222 GGATCAGGGGACCTTTGCTTTTATGATATCCACCGCTAGCAGTGGCGATTCAGGT 281
DB 41 GLYSERGLYGLYPROLEUPHEAPNAPLEUPROFOLASERSEGLYAPSERGLY 60
QY 282 TCTTCTGCACTCAATATCCAGATGTAAGATGMAAGGAGAAAGCAAGAGAA 341
DB 61 SERIUNALATHTSERILLESERDIMEVALYSTRGIVGIVLYSGLYVALIYAPRGLYS 80
QY 342 ACCTCCGAGAAAGAGAAATGGCAGTGAAGACTGTGTAAGAAAGATTGTAAAGCC 401
DB 81 THRSERGLIVGIVLVSGLYAPNAPLEUSERGIVGIVLVSGLYVALIYAPRGLYS 100
QY 402 TCTTGGTGTATCTTGTCTGAAGGGCTATGTGCTGACCGAGAGGAGTGAAGAGAG 461
DB 101 SERSERVALIIEPHEGLYLEULYSGLYTYRIVALAIAGIVARGLYGLYVARGIVGIV 120
QY 462 ATGCAGATGCCACGTCATCTCTGAACGACATCACCGAGAGTGAAGGCCCATCTGCC 521
DB 121 METGINAPRALIHLVALIILEULASNAPRIETRGIVGIVCYVARGPROPROSER 140
QY 522 CTCAATTCGCGGTTTCAATATTTTGTGTTTGTATGACATGAGAAATTTGAGCCCTCA 581
DB 141 LEULIETNARGVALSERLYRPHENALVALPHEAPRGLYHISGLYIILEYRGLASER 160
QY 582 AAATTTGCTGACAGAAATTTGCATCAAACTTAATCAGAAATTTCTTAAAGAGATGA 641
DB 161 LYSRPHENALAIAGIVLVSGLYSHILEULASNAPRIETRGIVGIVLVSGLYVALI 180
QY 642 ATCAGTGTAGAGAAACCGTGAAGAGATGCTTTTGGACACTTTTAAAGCATACTGATA 701
DB 181 ILESERVALGIVLVSSTRVALIYVARGCYSEULEUMAPNTRPHELYSHIETHRSPRGI 200
QY 702 GAGTCTTTAAACAAGCTTCAGACGAGAGCTGCTGGAAGAAGTGGTCCACTGCCAG 761
DB 201 GIVPHELEULYEGVINALASERSEGINLYSPROVALATRYAPBGILYSERTHRALATR 220
```

QY 762 TGTGTTCTGCTGTAGACACATCTTTATATTCACCACTCGGAGATGTCGGGCATC 821
DB 221 CysValLeuAlaValAspAsnIleuNyrIleAlaAsnLeuGlyAspSerArgAlaIle 240
QY 822 TTGTGTCGTTATATATGAGAGAGTCAAAAACATGACGCTTAAAGCTTCAGCAAAAGACAT 881
DB 241 LeuCysArgTyrAsnGluGluSerGlnLysHsiAlaIleuSerLeuSerLysGluHsi 260
QY 882 AATCAACTCAGTATGAAGACGCGATGAGATACAGAAAGCTGAGAAACGTACGAGAT 941
DB 261 AsnProThrGlnTyrGluGluArgMetArgIleGlnLysAlaGlyLysValArgAsp 280
QY 942 GGGCGTGTGTTGGGGGTGCTGAGAGTGTCAAGCTCCATTTGGGAGCGGCGAGTCAAGCGC 1001
DB 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyrLysArg 300
QY 1002 TGGGATGACCTGCTGTGCGCGAGATCAGACGCTGACCTGACCCCAATGACAGGTTG 1061
DB 301 CysGlyValIleThrSerValProAspIleArgArgCysGlnLysLeuThrProAsnAspArgPhe 320
QY 1062 ATTGTGTCGCTGTGAGTGGGCTGTCAAGCTCTTAAAGCTGAGAAAGACCGTGAAGTTC 1121
DB 321 IleuLeuAlaIleCysAspGlyLeuLeuLeuValPheThrProGluGluAlaValAsnPhe 340
QY 1122 ATCTGTCTCTGCTGTGAGATGAGAAAGATCCAGACCGGAGAGGAAAGTCCGACCGCGAC 1181
DB 341 IleuLeuSerCysLeuGluAspGluLysIleGlnThrArgGluGlyLysSerAlaAlaAsp 360
QY 1182 GCCCGTACGAAGACGCTGTGACAGAGCTGCGCCACAGAGCGGTCACGCGGAGCTCGGCC 1241
DB 361 AlaArgTyrGluAlaAlaCysAsnArgLeuAlaAsnLysAlaValaGlnArgLysSerAla 380
QY 1242 GACACGTCAGTGTATGTGTGTCGAGTACGAGTAC 1277
DB 381 AspAsnValThrValMetValValArgIleGlyHsi 392

RESULT 6
ABR05726
ID ABR05726 standard; Protein; 392 AA.
XX ABR05726;
AC ABR05726;
XX 30-APR-2002 (first entry)
XX
XX Human signal transduction protein clone tes3_31j20.
DB Human signal transduction protein clone tes3_31j20.
XX
XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
KM gene therapy.
XX
XX Homo sapiens.
OS
XX WO200198454-A2.
FN
XX 27-DEC-2001.
PD
XX 25-APR-2001; 2001WO-1B02050.
PF
XX 25-APR-2000; 2000US-199380P.
PR
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
PA
XX Wiemann S;
PI
XX WPI; 2002-055860/07.
DR
XX N-PSDB; ABA93763.
PT Human cDNA sequences and clones derived from human fetal brain, fetal
PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
PT screening and therapy -
XX
XX Claim 1; Page 377; 61pp; English.
XX
XX The present invention describes assemblages and computer readable media

CC comprising novel human cDNA sequences and clones derived from human
CC Foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
CC libraries. ABA93762 to ABA93766 represent human cDNA sequences from the
CC present invention which encode the proteins given in ABR05662 to
CC ABR05729. The human cDNA sequences and clones can be used in gene
CC therapy. The clones may be used in a variety of applications, for
CC example they may be used in profiling assays, for providing large arrays
CC of human genetic material for implementing large-scale screening
CC strategies and for treating diseases via gene therapy procedures.
XX
SQ Sequence 392 AA;
Alignment Scores:
Pred. No.: 2,31e-199 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: 23 Gaps: 0
US-09-935-124A-1 (1-1422) x ABR05726 (1-392)
QY 102 ATGGAACCTCTTCCGGGACCTGCGCGAGCGCTGCGCGCGCTGCGCGGAAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProAlaIleLys 20
QY 162 GAAGCTCAGAAAGACCCCTGCTCTTTGATGACCTCCCTCGGCGACGATGACTCA 221
DB 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerThrAspSer 40
QY 222 GGATCAGGAGGAGACCTTGTGCTTTTGTATGATCTCCACCGCTGACGATGCGCATTCAGGT 281
DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerThrAspSer 60
QY 282 TCTCTGTCACATCATATATCCAGATGATAAGCTAAAGGAAAGCAAGCAAGAAA 341
DB 61 SerLeuAlaThrSerIleSerGlnMetValIleThrGluGlyLysAlaLysArgLys 80
QY 342 ACCCGCAGGAAAGAAAGAAATGCGAGTGAAGCTTGTGAAAAGAAATTTGTAAGCC 401
DB 81 ThrSerGlnGlnGlnLysAsnGlySerGlnGlnLysValGlnLysValCysLysAla 100
QY 402 TCTTCGCGTATCTTGTGCTGTAAGGCTTATGCGTGAAGGATGAGGAGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGlnLysGlyLysGlnGln 120
QY 462 ATGAGAGATCCCAAGTCACTCTGAACGACATCAACGAGAGTGTAGGCCCATGCTCC 521
DB 121 MetGlnAspAlaHsiValIleLeuAsnAspIleThrGlnGlnCysArgProProSerSer 140
QY 522 CTCATTACTCGGCTTTCATATTTTCTGTTTGTATGATGAGATGAGAAATTCAGCTCA 581
DB 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHsiGlyLleArgAlaSer 160
QY 582 AAATTTGCTGACAGAAATTTGATCAAAATTAATCAGAAATTTCTTAAGAGATGTA 641
DB 161 LysPheAlaIleGlnAsnLeuHsiGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
QY 642 ATCAGTGAAGAAAACCGTGAAGAGATGCTTTTGAACCTTCAAGCATCTATGAA 701
DB 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHsiThrAspLys 200
QY 702 GAGTTCTTAAAGACCTTCCGACGAGAGCTGCTGAGAAAGTGGCTCACTGCGCAG 761
DB 201 GluPheLeuLysGlnLysLeuSerSerGlnLysProAlaIlePheAspGlySerThrAlaThr 220
QY 762 TGTGTCGTTATATATGAGAGAGTCAAAAACATGACGCTTAAAGCTTCAGCAAAAGACAT 821
DB 221 CysValLeuAlaValAspAsnIleuNyrIleAlaAsnLeuLysAspSerArgAlaIle 240
QY 822 TTGTGTCGTTATATATGAGAGAGTCAAAAACATGACGCTTAAAGCTTCAGCAAAAGACAT 881
DB 241 LeuCysArgTyrAsnGluGluSerGlnLysHsiAlaIleuSerLeuSerLysGluHsi 260

Qy	882	AAITCCAACTCACTGATGAAAGACCGGATAGAGATACAGAAAGCTGGAGAAACCTCAAGGAT	941
Db	261	AenProthrGlnTyrGlnGluArgMetCysAlaGlnIleValAlaGlyIleValIleValAlaArgSp	280
Qy	942	GGGCGTGTGTTGGGCGGCTGACTAGAGAGTGTCAAGCTCCACTTGGGGACGGGAGTACAAAGCGC	1001
Db	281	GlyArgValIleGlyValIleGluIleValIleSerArgSerIleGlyAspGlyValIleTyrValArg	300
Qy	1002	TGGCGTGCACCTGTGTGTGCCGACATCAGACGCTGCCAGCTGAACCCCAATGACAGGTTTC	1061
Db	301	CysGlyValIleThrSerValProAspIleArgArgCysGlnIleThrProAsnMetArgPhe	320
Qy	1062	ATTTTGTGGCTGTGATGGGCTTTTCAAGCTCTTTATCCCGAAGAAACCGTGAATCTT	1122
Db	321	IleLeuLeuAlaCysAspGlyLeuPheIleValPheThrProGlnIleValIleAlaAsnPhe	340
Qy	1122	ATCTGTCTCTCTCTCGAGGATGAAAGAAATCCAGACCCGGGAGGGGAATGCCACCGCAC	1181
Db	341	IleLeuSerCysLeuGluAspGlnIleValIleGlnIleThrArgGlnIleIlySerIleAlaAsp	360
Qy	1182	GCCGCTACGAAGACGCTTGCAACAGGCTGTCCCAACAGGCGGTGACAGCGGGGCTCGGCG	1241
Db	361	AlaArgTyrGlnIleAlaIleCysAsnArgLeuAlaAsnIleValIleGlnIleArgIleSerIleAla	380
Qy	1242	GACAACTGCTACTGTGATGTGTGTGTGGGATNAGGCGAC	1277
Db	381	AspAsnValIleThrValMetValIleArgIleGlyIleHis	392

the 500₂ nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03162 to AAH13528 and AAH13533 to AAH18742 represent human cDNA sequences; AA632446 to AA635893 represent human amino acid sequences; and AAH13529 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Alignment Scores:	
Pred. No.:	4,71e-199
Score:	2015.00
Percent Similarity:	100.00%
Best Local Similarity:	99.74%
Query Match:	78.71%
DB:	22
Length:	392
Matches:	391
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0

Db 201 GIuPheLeuLySGInAlaSerSerGInLySProAlaTPRlyASpGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCTGTAGACACATCTTTATATATTCACACCTCGAGATAGTCGGGCATC 821
Db 221 CyValLeuAlaValAlaSPasnIleLeuTyrlleAlaAsnLeuGlyASpSerArgAlaIle 240
Qy 822 TTGTGCTGTTATATAGAGAGAGTCAAAAAATCATGACCTTAAAGCTCAGCAAGAGCAT 881
Db 241 LeuCyArgTyrlAsnGluGluSerGInLySHeAlaAlaLeuSerLeuSerLyGluHis 260
Qy 882 AATCCAACTCAGTATGAGAGAGCGGATGATACAGAGCTGAGAGAAAATGTCAGGCAT 941
Db 261 AsnProThrGInTyGluGluArgMetArgIleGInLyAlaGlyGlyAsnValArgAsp 280
Qy 942 GGGCGTGTGTTGGGGGCTGAGAGTGTACAGCTCCATTTGGGAGCGGCATACAGCCG 1001
Db 281 GylArgValLeuGlyValLeuGluValSerArgSerIleGlyASpGlyGInTyrlLyArg 300
Qy 1002 TGGGCTGACCTCTGTGCTGCGGACATACAGCCGTGACCTACCCCAATGACAGCTTC 1061
Db 301 CyGlyValAlaThrSerValProAspIleArgArgCyGInLyAsnThrProAsnAspArgPhe 320
Qy 1062 ATTTGTTGGCTGTGATAGGCTCTTCAAGGCTTTTACCCCAAGAAAGCCGTGAACCTTC 1121
Db 321 IleLeuLeuAlaCyAspGlyLeuPheLyValPheThrProGluGluAlaValAlaAsnPhe 340
Qy 1122 ATCTTGCTCTGTCTCGAGAGTAAAGAATCCAGACCCGGGAAGGAGTCCGACCGGAC 1181
Db 341 IleLeuSerCyAlaLeuGluAspGluLyIleGInThrArgGluGlyLySerAlaAlaAsp 360
Qy 1182 GCCCGCTACAGACGACCTGCAACAGGCTGGCCACAGGCGGTGACCGGGCTCGGCC 1241
Db 361 AlaArgTyrlGluAlaAlaCyAsnArgLeuAlaAsnLyAlaValAlaGlnArgGlySerAla 380
Qy 1242 GACACGTCACCTGTGATGATGATGATGCGGATAGGGCAC 1277
Db 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 8
AAM38769
ID AAM38769 standard; Protein; 392 AA.
XX AC AAM38769;
XX DT 22-OCT-2001 (first entry)
XX DX Human polypeptide SEQ ID NO 1914.
KW Human; noctropic; immunosuppressant; cyostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
OS Homo sapiens.
XX
XX PN MO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000MO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0553117.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSB-) HYSBQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RP;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AA157925.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PS
PS Example 3; SEQ ID NO 1914; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic, or
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX SQ Sequence 392 AA;
XX
XX Alignment Scores:
Pred. No.: 5,986-199 Length: 392
Score: 2014.00 Matches: 391
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.74% Mismatches: 0
Query Match: 78.67% Indels: 0
DB: Gaps: 0

US-09-935-124A-1 (1-1422) x AAM38769 (1-392)

Qy 102 ATGACCTCTTTGGGGGACCTGCGCGAGCCGAGCCGCTCGCGCGCCGGCTCGCGGAAA 161
Db 1 MetAspLeuPheGlyAspLeuProGluProGluThrArgProAlaAlaGlyHis 20
Qy 162 GAAAGCTCAAGAAAGACCCCTGCTCTTTGATGACCTCTCTCGCGCCAGCATGACTCA 221
Db 21 GluAlaGlnLySgLyProLeuLeuPheAspAspLeuProAlaSerSerThrAspSer 40
Qy 222 GGATCAGGGGAGACCTTTGCTTTTGTATGATCTCCACCGCTGACAGTGGCATTCAGGT 281
Db 41 GlySerGlyGlyProLeuLeuPheAspAspLeuProProAlaSerSerGlyAspSerGly 60
Qy 282 TCTCTTGCCACATCAATATCCAGATGCTAAAGACTGAAGGAAAGAAAGCAAGAGAAA 341
Db 61 SerLeuAlaThrSerIleSerIleSerGlnMetValylThrGlnGlySgLyAlaLyAsArgHis 80
Qy 342 ACCCTCGAGAGAGAGAAAGATGAGCAGTGAAGGCTGTGAGAAAAGATTTGTAAACC 401
Db 81 ThrSerGluGluGluLySAsnGlySerGlnLeuValGlnLySgLyValCysLySAla 100
Qy 402 TCTTCGCGATCTTTGCTGCTGAAGGGCTAGTGGCTGAGGGAAGGTTAGAGGAG 461
Db 101 SerSerValIlePheGlyLeuLySgLyTyrlAlaAlaGluArgSgLyGlnArgGlnGlu 120
Qy 462 ATGACAGATGCCCACTGATCTCTGAACGATGACGAGAGAGTGTGGCCCACTGCC 521
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGlnGluCysArgProProSerSer 140
Qy 522 CTCATTACTGGGTTTCATATTTTCTGTTTGTATGACATGAGAGAAATTCAGACCTCA 581
Db 141 LeuIleThrArgValSerTyrlPheAlaValAlaPheAspGlyHisGlyGlyIleArgAlaSer 160

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QY 582 AATTGCTGCACAGAAATTGTCATCAAAAATTATATGAAAAATTCTTAAAGAGATGTA 641
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PI LysPheAlaIaIaGlnAenLeuHISGlnAenLeuIleArgLysPheProLysGlyAAspVal 180
Db 161 LysPheAlaIaIaGlnAenLeuHISGlnAenLeuIleArgLysPheProLysGlyAAspVal 180
QY 642 ATCAGTGTGAGAAAAACCGGAGAGATGCTCTTTGGACACTTTCAAGCTTACTGATGAA 701
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PI LysSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHISLSTHAspGln 200
Db 181 LysSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHISLSTHAspGln 200
QY 702 GAGTTCCTTAAACAGCTTCCAGCCAGAACCTGCTGGAAGAAGAGGATCCATGCACAG 761
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PI GluPheLeuLysGlnIleAspSerGlnLysProAlaIlePheLysPheLysSerThrAlaThr 220
Db 201 GluPheLeuLysGlnIleAspSerGlnLysProAlaIlePheLysPheLysSerThrAlaThr 220
QY 762 TGTGTTCTGGCTGTAGCAACATTTTATATATGCAACCTCGAGATAGTGGGCAATC 821
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PI CysValLeuAlaValAlaAspAenIleLeuYrIleAlaAenLeuLysPheSerArgAlaIle 240
Db 221 CysValLeuAlaValAlaAspAenIleLeuYrIleAlaAenLeuLysPheSerArgAlaIle 240
QY 822 TTGTGCTGTTATATAGAGAGATCAAAAAATGCAAGCCCTTAAGCCTTCAAGCAAAAGCAT 881
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PI LeuCysArgGlyAsnGlnGlnSerGlnLysHISAlaIleLeuSerLeuSerLysGlnHIS 260
Db 241 LeuCysArgGlyAsnGlnGlnSerGlnLysHISAlaIleLeuSerLeuSerLysGlnHIS 260
QY 882 AATCAACTCAGTATGAGAGAGAGATGAGATACAGAGAGCTGAGAGAAAGTCAGAGAT 941
XX |||
PI AsnProThrGlnIryGlnGlnLysMetArgIleGlnLysAlaIleGlyLysAsnValArgAsp 280
Db 261 AsnProThrGlnIryGlnGlnLysMetArgIleGlnLysAlaIleGlyLysAsnValArgAsp 280
QY 942 GGGCGTGTGGGCGCTGCTAGAGAGGTGTCAAGCTCCATTGGGAGCGGCGATCAAGCCG 1001
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PI GlyArgValLeuGlnValLeuGlnValLysArgSerIleGlyLysPheGlnIryLysArg 300
Db 281 GlyArgValLeuGlnValLeuGlnValLysArgSerIleGlyLysPheGlnIryLysArg 300
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PI CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
Db 301 CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
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XX |||
PI IleLeuLeuAlaCysAspGlyLeuPheLysValLysPheThrProGlnGlnValAlaAsnPhe 340
Db 321 IleLeuLeuAlaCysAspGlyLeuPheLysValLysPheThrProGlnGlnValAlaAsnPhe 340
QY 1122 ATCTGTCTCTGCTGCTGAGATGAAAGATCCAGACCCGGGAGAGAAAGTCCGACGCCAG 1181
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PI IleLeuSerCysLeuGlnAspGlnLysIleGlnThrArgGlnLysSerAlaIaIaGln 360
Db 341 IleLeuSerCysLeuGlnAspGlnLysIleGlnThrArgGlnLysSerAlaIaIaGln 360
QY 1182 GCGCGCTAGCAAGACGCTGCAACAGGCTGCGCAACAGCGGCTGACGGGCTGGGCC 1241
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Db 361 AlaArgTyrGlnLysAlaIaCysAsnArgLeuAlaAsnLysAlaValGlnArgLysSerAla 380
QY 1242 GACCAAGTCACTGATGATGGTGGTGGGATAGGGCAC 1277
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RESULT 9
ABG09937
ID ABG09937 standard; Protein; 378 AA.
XX
AC ABG09937;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9928.
XX
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX
DE food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
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PA (HSE-) HISEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
DR N-PsDB; AAS74124.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
PS Claim 20; SEQ ID No 40296; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcc_sequences.
XX
XX SQ Sequence 378 AA:
XX
XX Alignment Scores:
XX Pred. No.: 2,07e-141 Length: 378
XX Score: 1457.50 Matches: 303
XX Percent Similarity: 81.23% Conservative: 13
XX Best Local Similarity: 77.89% Mismatches: 46
XX Query Match: 56.93% Indels: 27
XX DB: 22 Gaps: 6
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QY 159 AAGAAGCTCAGAAAGAACCCCTGCTTTTGTATGACTTCCTCCGGCAGACGTAAGTAC 218
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Db 1 LysGlnAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAsp 20
QY 219 TCAGAGTACAGGGGACCTTGTCTTTTATGATATCTCCACCCCGCTAGCAGTGGCATTC 278
XX |||
Db 21 SerAla-----ValAlaIleLeuGlnLysThr 29
QY 279 GGTTCCTTGGCCATCAATATCCAGATGTAAAGACTGAAGGAAAGCAAGCAAGA 338
XX |||
Db 30 ProSerProValThrLeuThrPheLeuGlnThrArgArgLysLysLysLysLysLysLys 49
QY 339 AAACCTCCGAGAAAGAGAGATGAGAGCTGTTGGTGAAGAAAGAAAGTGTGAAA 398
XX |||
Db 50 SerLeuAspTyrGlnSerLysValGlnLysLysProTyrCysHISGlnLysGlnLys 69
QY 399 -----GCTCTTGGTATCTTTGGTCTG 422
XX |||
Db 70 AlaAspArgPheLeuGlnLysArgGlyArgValProAlaSerSerValIlePheGlnLys 89
QY 423 AAGGCTATGTTGGCTGAGCGGAAAGGTGAGAGAGAGATGACAGATGCCCATCATC 482
XX |||
Db 90 LysGlyTyrValAlaGlnArgLysGlyGlnArgGlnGlnLysMetGlnAspAlaIleValIle 109
QY 483 CTGAACGACATCACCGAAGAGTGAAGCCCGCATGCTCCATTAATTCGGGTTTCATAT 542
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QY 312 AAGACTGAAGGAAAGAGCAAAAGAAAACTCCGAGAGAGAGAAATGGCACTGAA 371
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 CC |||||
 QY 372 GAGCTTGGAAGAAAGAAAGTTTAAAGCCTCTTCGTGATCTTTGGTCTGAAGGCTAT 431
 CC |||||
 Db 128 GtLeuValaGlulYalYalValCysLysAlaSerSerValIlePheGlyLeuYsgLYTyr 147
 CC |||||
 QY 432 GTGGCTGACGGAAGGCTGAGAGAGAGATGACAGATGCCACCTCATCTCGAAGCAG 491
 CC |||||
 Db 148 ValAlaGlulYalYalYsgLYalYalGluGluMeGlnPheAlaHisValIleLeuAenAap 167
 CC |||||
 QY 492 ATCACCAGAGAGTGTAGAGCCCATGCTCTCATTAATCTCGGCTTCATATTTGCTGT 551
 CC |||||
 Db 168 IleThrglUGlUGlyArGPrProSerSerLeuIleThrArGValSerYrPheAlaVal 187
 CC |||||
 QY 552 TTGTGAGCATGAGAGAAATTCAGAGCTCAAAATTTGCTGCACAGAAATTTGCATCAAAAC 611
 CC |||||
 Db 188 PheAspGlyHisGlyglYleArGAlaSerLysPheAlaIleGlnsnLeuHisGlnAen 207
 CC |||||
 QY 612 TTAATCAGAAAAATTTCTTAAAGAGATGTATCAGTGTAGAG 653
 CC |||||
 Db 208 LeuIleArGLyPheProLYsgLYaAspValIleSerValGlu 221
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 RESULT 11
 ABG07619
 ID ABG07619 standard; Protein; 211 AA.
 XX
 AC ABG07619;
 DT 13-FEB-2002 (first entry)
 DE
 XX Novel human diagnostic protein #7610.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT.
 XX
 DR MPI: 2001-639362/73.
 DR N-PSDB; AAS71806.
 XX
 PT New isolated polynucleotide and encoded polypeptide, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 Claim 20; SEQ ID No 37978; 103bp; English.
 CC
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 211 AA;

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
5,33e-46	211	124	54	13	5
Score:	533.50	Conservative:	11		
Percent Similarity:	66.83%	Mismatches:	54		
Best Local Similarity:	61.39%	Indels:	13		
Query Match:	20.84%	Gaps:	5		
DB:	22				

US-09-935-124A-1 (1-1422) x ABG07619 (1-211)

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 QY 759 ACGTGTTCTGCGTGTAGACAACATTCCTTATTTGCAACCTCGAGATGTGGGCA 818
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 Db 30 SerValaGlnValIleThlyeProArGLyLeuTrpProGlnTrpIleGlnHisArGAla 49
 CC |||||
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 Db :|||
 Db 50 ArgArGProCysLeuGlnGlnAlaProCysSerSerArGProHisAlaProAlaSerLeu 69
 CC |||||
 QY 870 ACCAAAGACATATATTCACATCAGATGAGAGCGGATGAGATCAG----- 917
 Db :|||
 Db 70 ProProSerSerSerProThrAlaArGAspThrLysHisArGAlaGlnValYsThrThr 89
 CC |||||
 QY 918 AAGGCTGAGAAAGGTGACGAGTGGGCGCTGTTGGGCGTCTAGAGGTGCAGGCTCC 977
 Db :|||
 Db 90 AspSerGlyAlaArGLyArGLyAspGlyArGLyValLeuGlyValLeuGlnValSerArGSer 109
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 QY 978 ATTGGGAGCGGCGAGTACAGAGCGCTGCGGTGCACCTCTGTGCGCCGAGATCAGAGCTGCG 1037
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 Db 110 IleAlaAspGlyGlnTrlyArGLyArGLyValThrSerValProAspIleArGLyArGLy 129
 CC |||||
 QY 1038 CAGCTGACCCCAAT--GACAGGTTCAATTTGTTGGCTGTGATGGGCTCTTCAAGCTC 1094
 Db :|||
 Db 130 GlnLeuTrpProGln**ProGlySerIleLeuLeuAlaCysAspGlyLeuPheYsVal 149
 CC |||||
 QY 1095 TTTACCCCGAAGAGCGGTGAATCTTCACTGCTGCTGCTGAGAGGAGAAAGATCCGAG 1154
 Db :|||
 Db 150 PheTrpProGlnGlnAlaValaAsnPheIleLeuSerCysLeuGlnAspGlnYsIleGln 169
 CC |||||
 QY 1155 ACCCGGAGGAGAGTCCGACGCGCCGCTACGAGACGCTGCAACAGGCTGGCC 1214
 Db :|||
 Db 170 ThrArGLyGlnYlYsSerAlaAlaAspValArGLyTrGlnAlaAlaCysAsnMetLeuAla 189
 CC |||||
 QY 1215 AACAAAGCGGTGACAGCGGGCTCG--GCCGACAACGTCACTGTATGTGTGGCGGATA 1271
 Db :|||
 Db 190 AsnYsAlaValaAlaAlaGlyAlaArGLyProAspAenValThrValMetValValArGLy 209
 CC |||||
 QY 1272 GGGCAC 1277
 Db :|||
 Db 210 GlyHis 211
 CC |||||
 RESULT 12
 AAU23252
 ID AAU23252 standard; Protein; 138 AA.
 XX
 AC AAU23252;

XX 18-DEC-2001 (first entry)
DT
XX
XX Novel human enzyme polypeptide #338.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KM ligase; hyperproliferative disorder; immunodeficiency disorder;
KM autoimmune disorder; neurological disorder; metabolic disorder;
KM inflammatory disorder; cardiovascular disorder; reproductive disorder;
KM blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KM nephrotropic; anticoagulant.
XX
OS Homo sapiens.
PN WC200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JUN-2001; 2001WO-US01239.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 18-APR-2000; 2000US-0198123.
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PR 23-AUG-2000; 2000US-0227009.
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PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
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PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237027.
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PR 02-OCT-2000; 2000US-0237029.
PR 02-OCT-2000; 2000US-0237030.
PR 13-OCT-2000; 2000US-0238935.
PR 13-OCT-2000; 2000US-0238937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241809.
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PR 20-OCT-2000; 2000US-0241826.
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PR 05-DEC-2000; 2000US-0251030.

PR 08-JUN-1999; 99US-0138094.
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PR 20-JUL-1999; 99US-0144632.
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US-09-935-124a-1 (1-1422) x AAG18068 (1-295)

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AC AAG18067;
DT 17-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
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PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity: 38.01% Mismatches: 65
Query Match: 15.29% Indels: 17
DB: Gaps: 6
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US-09-935-124A-1 (1-1422) x AAG18069 (1-219)

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DB 1 MetGluAspValItrpValIleuProAspAlaSerLeuAspHe-----ProGlyThr 18
OY 522 CTCATTACTCGGGTTTCATATTTGCTTTTGTATGATGACAGAGAAATTCAGAGCTCA 581
DB 19 Leu-----ArgCysAlaHisPheAlaIleItyrAspGlyHisGlyItyrGluAlaLa 36
OY 582 AATTTGCTGCACAGAAATTTGCATCAAACTTATCAGAAATTTCTTAAGGAGATGTA 641
DB 37 GluPheAlaIleLysHisIleuHisLeuAsnValLeuSerAlaGlyLeuProArgGluLeu 56
OY 642 ATCAGTGTAGAGAAAACCTGAAGAGATGCTTTTGACACTTTCAGACATACTGATGA 701
DB 57 LeuAspVal---LysValAlaLysLysValAlaIleLeuGluGlyPheArgLysThrAspGlu 75
OY 702 GAGTTCCTTAACACAGCTCCAGCCAGAACCCGCTCGAAGAAATGGTCCACTGCCACG 761
DB 76 LeuLeuLeuGlnLysSerValSer-----GlyGlyItrpGlnAspIlyAlaThrAlaVal 93
OY 762 TGTGTTCTGCTGTGTAGCAACAATCTTTATATGACCACTCGAGATGATGCGGCAATC 821
DB 94 CysValItrpIleLeuAspGlnLysValAlaPheValAlaAsnIleGlyLysPalaLysAlaVal 113
OY 822 TTGTGTCGT-----TATATAGGAGAGAGTCAAAAAACAT 854
DB 114 LeuAlaArgSerSerThrItrpAsnGluLeuGlyAsnHisThrGlnIleGlyLysAsnProLeu 133
OY 855 GAGGCTTAAAGCTTCAGCAAAAGCATATCCAACTCAGTATGAGAGAGGAGATGAGATA 914
DB 134 LysAlaIleValLeuThrArgGlnHisLysValAlaIleItyrProGlnIleuArgSerArgIle 153
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DB 154 GlnLysSerGlyGlyValIleSerSerAsnGlnItyrGluLeuGlnGlyArgGluIleValSer 173
OY 972 CGCTCATTTGGGAGCGGAGACATCAAGCGCTCGCTGTCACCTGTGTGCCACATCAGA 1031
DB 174 ArgAlaPheGlyLysPArgHisPheLysLysPheGlyValSerAlaThrProAspIleHis 193
OY 1032 CGCTGCAGCTGACCCCAATGACAGGTTTCATTTTGTGGCTGTGATGAGGCTTTCAG 1091
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OY 1092 GTC 1094
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AC ABR77579;
DT 02-SEP-2002 (first entry)
DE Physcomitrella patens PP2C-1 SEQ ID NO 14.
KW Physcomitrella patens; PHSRP; phosphatase stress related protein;
PP2A; PP2C; enzyme; transgenic; plant; stress tolerance.
OS Physcomitrella patens.
PN WO200246442-A2.
PX 13-JUN-2002.
PF 06-APR-2001; 2001WO-US11253.
PR 07-APR-2000; 2000US-196001P.
PA (BADI ) BASF PLANT SCI GMBH.
PI Da Costa ESO, Bohmert HJ, Ishitani M, Van Thieljen N, Chan R;
DR WPI; 2002-508562/54.
N-PSDB; ABR81333.
XX New transgenic plant cell transformed by phosphatase stress-related
PT protein coding nucleic acid whose expression in the cell results in
PT increased tolerance to environmental stress compared to wild type cell
PS -
XX Claim 16; Fig 3; 106pp; English.
XX The invention relates to a transgenic plant cell (I) transformed by a
XX phosphatase stress-related protein (PHSRP) coding nucleic acid
XX (ABR81330-ABR81334), where expression of the nucleic acid in the plant
XX cell results in increased tolerance to an environmental stress as
XX compared to a wild type variety of the plant cell. PHSRP encoding genes
XX are useful for identifying Physcomitrella patens and related organisms,
XX as markers for specific regions of the genome, mapping of genomes of
XX organisms related to P. patens, identification and localisation of P.
XX patens sequences of interest, evolutionary studies, determination of
XX PHSRP regions required for function, modulation of a PHSRP activity,
XX modulation of the metabolism of one or more cell functions, modulation
XX of the transmembrane transport of one or more compounds and modulation
XX of stress resistance. The gene is also useful for identifying and/or
XX cloning PHSRP homologues in other cell types and organisms, for
XX identifying an organism as being P. patens or its close relative and for
XX evolutionary and protein structural studies. The present sequence is that
XX of a PHSRP of the invention.
XX Sequence 353 AA;
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Alignment Scores:

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Percent Similarity:	43.78%	Conservative:	60
Best Local Similarity:	28.24%	Mismatches:	98
Query Match:	14.67%	Indels:	119
DB:	23	Gaps:	12

US-09-935-124a-1 (1-1422) x ABB7579 (1-353)

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QY 459 GAGATGACAGATGCCACGTCATCTGTAACGATCAGCAGAGAGTGAAGCCCATCG 518
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DB 50 -----ThySerThrSerIlePheArgGlyHisGlyLysLeuVal 66
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DB 87 GlyAsp-----LeuLysAlaSerLeuGluTyrSerPheLeuArg 99
QY 693 ACTGATGAA-----GAGTTCCTTAAACAGCT 719
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DB 100 MetArgGluMetMetLysGlyAlaSerGlyTyrPylGluLeuGlnSerLeuGlnGluThr 119
QY 720 TCCAGCCAG----- 728
DB 120 SerSerGlnLeuAspLysLeuGlyAsnGlyAsnSerSerSerAsnAlaArgGluAspAsp 139
QY 728 ----- 728
DB 140 GluSerAspLysSerTyrAlaValLeuThrGluSerAsnAspSerAsnLeuAlaThrLys 159
QY 729 AAGCTGCTGGAAGAT-----GGGTCCACTGCCACCTGTGTTCTG 770
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DB 160 LysHisLysTyrSerAspPheGlnGlyProIleTyrGlySerThrAlaValAlaLeu 179
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DB 180 IleArgGlyAsnLysLeuPheValAlaAsnAlaGlyAspSerHisCysIleMetSerArg 199
QY 831 TATPATGAGAGAGTCAAAACATGACGCTTAAGCTGACGAGAGAGCATATATCAACT 890
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DB 200 ArgGlyGlu-----AlaValAsnLeuSerIleAspHisLysProAsn 213
QY 891 CAGTATGAGAGAGCGATGAGATACAGAAAGCTGAGAGAAAGTCAGGAGGGCGTGT 950
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DB 214 LeuGluHisGlnArgLysArgLysLeuSerAlaIleGlyAspMetGlnPheLysHisGlyArgVal 233
QY 951 TTGGCGCTGTAAGGTTGACGCTCCATTGGGAGCGGAGCATACAG----- 998
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DB 234 AsnGlySerLeuAsnLeuThrArgAlaIleGlyAspMetGlnPheLysHisGlyArgProAsp 253
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DB 254 LeuProArgAspLysGlnValAlaValThrCysArgProAspValAlaGluValAspLysGly 273
QY 1047 CCCAATGACAGGTTCAATTTGTTGGCTGTGATGGGCTCTTCAAGGCTTTTACCAGCAA 1106
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DB 274 ProGlyAspGluPheIleValLeuAlaCysAspGlyIleTyrAspValMetSerSerGln 293
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DB 294 AlaValAlaAspPheValLysSerArgLeuProThrThrLys----- 307
QY 1167 AAGTCCGACCGACCCCGCTACGACACCTGCAACAGCTGCGCCAAAGCGCGTGG 1226
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DB 308 -----ThrLeuSerSerLeuCysGlnGluIleLeuAspTyrCysLeu 321
QY 1227 -----CAGCGGGGCTCGGCGCAGACGTCACCTGATGAGTGGTGGCGATA 1271
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AC AAG16902;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.:	1,37e-28	Length:	383
Score:	366.50	Matches:	112
Percent Similarity:	50.15%	Conservative:	59
Best Local Similarity:	52.84%	Mismatches:	109
Query Match:	14.32%	Indels:	61
DB:	21	Gaps:	13

US-09-935-124A-1 (1-1422) x AAG18039 (1-383)

QY 291 ACATCAATRTCCAGATGGTAAAGACTGAAGGAGAAAGACAAAGAGAAAACTTCGAG 350
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:::~::

D	21	ThrsrAlaIyMeMeValAspThr-----SerAlaGly 32	XX	AA39774;	
Q	351	GAAGAGAATGCGAGCTTGGAAGAAAGATTGTAAGCCTTCGGTG 410	AC	18-OCT-2000 (first entry)	
D	33	GlulysArgIleSerIeuValAspMetProProGluValAspArgGlyIle 52	DT	Arabidopsis thaliana protein fragment SEQ ID NO: 49264.	
Q	411	ATCTTGTCGTAG-----GGTATGCGCTGACGGAG 446	DE	Protein identification; signal transduction pathway;	
D	53	GlyGlyIleTyrIleAsnAspAspGlySerIeuSerCysGlyTyrCysSerPheArg--- 71	XX	hybridisation assay; genetic mapping; gene expression control; promoter;	
Q	447	GGTGAAGGAGAGATGACAGATGCCAGCTCATCTTAAGACATACCGAGAGATG 506	KW	termination sequence.	
D	72	GlyLysArgSerThreGluAspPheArgIleLysAlaSerThrIleGlyIle--- 90	XX	Arabidopsis thaliana.	
Q	507	AGGCCCCATCGTCCCTCATTACTCGGGTTTCATATTTGCTGTTTGTATGACATGA 566	XX	EP1033405-A2.	
D	91	-----GlnAlaValCysMetPheGlyIlePheAspGlyIleGly 103	PN	06-SEP-2000.	
Q	567	GAATTCAGCCTCAAAATTTGTCACAGAAATTTGCATCAAACTTAATCAGAAATTT 626	PD	25-FEB-2000; 2000EP-0301439.	
D	104	GlySerArgAlaIleGlyTyrIleuLysGluIleLeuPheAsnAsnIleuMet---LysHis 122	XX	25-FEB-1999; 99US-0121825.	
Q	627	CCTAAAGAGATGTATCATCATGTAGAGAAACCGTGAAGATGCCCTTTGACACATTC 686	PR	05-MAR-1999; 99US-0123180.	
D	123	ProGln-----PheLeuThrAspThrIleLysAlaIleuAsnGluThrTyr 137	PR	09-MAR-1999; 99US-0123548.	
Q	687	AACATATCTATGATGAAGATCCTTAACAAGCTTCCAGCAGAGCCTGCTGGAA--- 743	PR	23-MAR-1999; 99US-0125788.	
D	138	LysGlnThrAspValAlaPheLeuGlu-----SerGluLysAspThrTyrArgAsp 154	PR	25-MAR-1999; 99US-0126264.	
Q	744	GATGGTCACCTGCGACGCGTTCCTGCTGTAGACAACTTATATATGCGAACCTC 803	PR	29-MAR-1999; 99US-0126785.	
D	155	AspGlySerThrIleSerIleAlaValIleuValGlyAsnHisIleuTyrValAlaHisVal 174	PR	01-APR-1999; 99US-0127462.	
Q	804	GAGATATGTCGGCAATCTTGTGTCGTTAATGAGAGATCAAAAATGCAAGCCTTA 863	PR	06-APR-1999; 99US-0128234.	
D	175	GlyAspSerArgThrIleVal-----SerLysAlaGlyLysValIle 188	PR	08-APR-1999; 99US-0128714.	
Q	864	AGCCTGACAAAGCATTAATCCACTCAGTATGAAGACCGATGAGATACAGAGCTT 923	PR	16-APR-1999; 99US-0129845.	
D	189	AlaIeuSerAspAspHisLysPheAsnArgSerAspGluArgLysArgIleGluSerAla 208	PR	19-APR-1999; 99US-0130077.	
Q	924	GAGAGAAACGTCAAG-----GATGGCGTGTGTTGGGGCTCTAGAGTGTCAAGC 974	PR	21-APR-1999; 99US-0130449.	
D	209	GlyGlyValIleMetTyrAlaGlyThrTyrArgValGlyIleValIleuAlaMetSerArg 228	PR	23-APR-1999; 99US-0130510.	
Q	975	TCCATTGGGAGCGGCGACAGACGCGTGCAGTGCACCTCTGTCCGACATCAGACGC 1034	PR	28-APR-1999; 99US-0131448.	
D	229	AlaPheGlyAsnArgMetIleuLysGlnPhe---ValValAlaGluProGluIleGlnAsp 247	PR	30-APR-1999; 99US-0132048.	
Q	1035	TGCCAGCTGACCCCCAATGACAGGTTCAATTTGTGGCCGTGATGGGCTTCAAGTTC 1094	PR	04-MAY-1999; 99US-0132484.	
D	248	LeuGluIleAspHisGluAlaGluIleuLysValIleuAlaSerAspGlyLeuTyrAspVal 267	PR	05-MAY-1999; 99US-0132485.	
Q	1095	TTTACCCCAAGAAAGCCGTGAATCTATCTGTCCCTGCTGACAGAGAAATCAG 1154	PR	06-MAY-1999; 99US-0132486.	
D	268	ValProAsnGluAspAlaVal-----AlaIleuAlaGlnSerIleGluGlnPro----- 283	PR	07-MAY-1999; 99US-0132487.	
Q	1155	ACCCGGGAAGGAGATCCGACCGCAGCCCGCTAGAGACGACCTGCAACAGCCTGGCC 1214	PR	11-MAY-1999; 99US-0132863.	
D	284	-----GlnAlaAlaAlaArgLysLeuThr 291	PR	14-MAY-1999; 99US-0134218.	
Q	1215	AACAAGCGGTGACGGGGGCTCGCCGACACATCATGTATAGTGTGCGATGAGG 1274	PR	14-MAY-1999; 99US-0134219.	
D	292	AspThrAlaPheSerArgGlySerIleAspAsnIleThrCysIleValValLysPheArg 311	PR	14-MAY-1999; 99US-0134221.	
Q	1275	CAC 1277	PR	14-MAY-1999; 99US-0134370.	
D	312	His 312	PR	18-MAY-1999; 99US-0134768.	
RESULT 21			PR	19-MAY-1999; 99US-0134941.	
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			PR	24-MAY-1999; 99US-0135629.	
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			PR	27-MAY-1999; 99US-0136392.	
			PR	28-MAY-1999; 99US-0136788.	
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			PR	14-JUN-1999; 99US-0139119.	
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			PR	18-JUN-1999; 99US-0139455.	
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PR 09-AUG-1999; 99US-0147493.
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PR 14-OCT-1999; 99US-0159638.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 1,45e-28 Length: 420
Score: 366.50 Matches: 112
Percent Similarity: 50.15% Conservative: 59
Best Local Similarity: 32.84% Mismatches: 109
Query Match: 14.32% Indels: 61
Dels: 21 Gaps: 13

US-09-935-124A-1 (1-1422) x AAC39774 (1-420)

QY 291 ACATCAATATCCAGATGTGAAGCTGAGGAAAGAGCAAGAAAACCTCCGAG 350
Db 58 ThrSerAlaIysMetMetValAspThr-----SerAlaGly 69
QY 351 GAAGAGAAGATGCGAGTGTGTGAAAGAAAGTTGTAAAGCCCTTCGGTG 410
Db 70 GIuLySArgIleSerLeuValAspMetProProGIuLySValAspAspGlyIyTrIle 89
QY 411 ATCTTGTGCTGAG-----GGCTATGTGCTGAGCGGAAG 446

Db	90	GLYGLYGLYTRPLeuAsnAspArgGlySerLeuSerGlyTyrCysSerPheArg----	108
Qy	447	GGTGAAGGAGGAATATGACAGATGCGCCAGTCACTCGTAAGACATCGACCGAGAGTGT	506
Db	109	GLYAsnArgSerThrMetGluAsnPheArgLysLeuValSerThrIleGluGly---	127
Qy	507	AGGCGCCCATCGTCCCTCATCTACGCGGTTTCATATTTGCTGGTTTGAATGACATGGA	566
Db	128	-----GlnAlaValaCysMetPheGlyIlePheArgGlyAsnGly	140
Qy	567	GGATATTCAGCTCAAAATTTGCTGCACAGACATTTGGCATCAAACTTATACGAAATTT	626
Db	141	GLYSerArgAlaIleGlyTyrLeuValGluHisIlePheAsnAlaMetMet---LysHis	159
Qy	627	CTTAAAGAGATGATATCATGATGAGAGAAAACCTGAAGAGATGCTTTTGGACACTTTC	686
Db	160	ProGln-----PheLeuThrAspThrLysLeuAlaLeuAsnGluThrTyr	174
Qy	687	AAGCATATTCATGAAGAGTTCTCTTAAACAAGCTTCCAGCGAAGACCTGCTGGAAA---	743
Db	175	LysGlnThrAspValAlaPheLeuGlu-----SerGluLysAspThrTyrAsnArg	191
Qy	744	GATGGGTCACATCGCCACGCTGGTGTCTGCTGTAGCAACATCTTTATTTGGCAACCTC	803
Db	192	AspGlySerThrAlaSerAlaIleValLeuValGlyAsnHisIleGlyValAlaAsnVal	211
Qy	804	GGAGATATTCGCGCAATCTGTGTGCTGTTAATGAAGAGAGTCAAAACATGACGCTTA	863
Db	212	GLYAspSerArgThrIleVal-----SerLysAlaGlyLysAlaIle	225
Qy	864	AGCTTACGCAAGACATTAATTCGAATCTCAATGAAAGACGGATGAGATATCAAAAGCTT	923
Db	226	AlaLeuSerAspPheIleLysArgAsnArgSerAspGluArgLysGlyIleGluSerAla	245
Qy	924	GGAGGAAGCTGACG-----GATGCGCTGTTTGGCGCTGTCAGAGTGTACCC	974
Db	246	GLYGLYValIleMetThrAlaGlyLysThrTyrArgValGlyGlyValLeuAlaMetSerArg	265
Qy	975	TCCATTGTGGGACGGGACAGTACAGACGGCTGCGATGTCACTCTGTGCCCGACATCAGACG	1034
Db	266	AlaPheGlyLysAsnArgMetLeuLysGlnPhe---ValValAlaGluProGluIleGlnAsp	284
Qy	1035	TGCGACGTACACCCCAATGACAGAGGTTCAATTTGTGGCTGTGATGAGGCTCTTCAAGTTC	1094
Db	285	LeuGlnIleAspHisGluAlaGluIleLeuValLeuAlaSerAspGlyLeuTyrAspVal	304
Qy	1095	TTTATCCCAAGAAAGACCGTAACTCATCTTGTCTGCTGTGCGAGATGAAGAAGATCCAG	1154
Db	305	ValProAsnGluAspAlaVal-----AlaLeuAlaGlnSerGluGluGlnPro-----	320
Qy	1155	ACCGGGAGAGGAGATCGGACGCGACGCGCTGACGAAGACGAGCTGACAGACGCTGGCC	1214
Db	321	-----GluAlaIleAlaIleArgLysLeuThr	328
Qy	1215	ATCAAGGCGGTGCACGCGGGCTGCGCGCGCAACATCACTGAATGATGTGTGGCGAGATGGG	1274
Db	329	AspThrAlaPheSerArgGlySerAlaAspAsnIleThrCysIleValValLysPheArg	348
Qy	1275	CAC 1277	
Db	349	His 349	
RESULT 22			
AB08398			
ID	AB08398	standard; Protein; 454 AA.	
AC	AB08398;		
XX	16-MAY-2002	(first entry)	
DT			
XX	Human-derived protein phosphatase.		
DE			

KW Human: protein phosphatase; calmodulin-dependent phosphoenzyme II;
 XX phosphorylation.
 OS Homo sapiens.
 XX
 XX JP2001333776-A.
 XX
 XX 04-DEC-2001.
 XX
 XX 25-MAY-2000; 2000JP-0154223.
 XX
 XX 25-MAY-2000; 2000JP-0154223.
 XX
 XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
 XX PA (SUNR) SUNTORY LTD.
 XX
 XX WPI; 2002-135942/18.
 XX DR N-PSDB; ABA97280.
 XX
 XX A human-derived protein phosphatase and its inhibitor -
 XX
 XX Claim 1; Page 8-9; 15pp; Japanese.
 XX
 XX The invention relates to a human-derived protein phosphatase which has
 CC protein phosphatase activity, in which the dephosphorylating amino acid
 CC is threonine-specific, which requires Mg^{2+} for the dephosphorylating
 CC reaction. The therapeutic agent of the invention can be used for the
 CC diseases caused by inactivation of calmodulin-dependent phosphoenzyme II.
 CC The current sequence represents a human-derived protein phosphatase.
 XX
 XX Sequence 454 AA;
 SQ
 Alignment Scores:
 Pred. NO.: 1.51e-28 Length: 454
 Score: 366.50 Matches: 127
 Percent Similarity: 42.86% Conservative: 63
 Best Local Similarity: 28.35% Mismatches: 145
 Query Match: 14.32% Indels: 111
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 Db 6 ProGlnLysSerSerProMetAlaSerGlyAlaGlnGluThrProGlyPheLeuAspThr 25
 QY 183 CTTGTTGAAGACCTCCCTCCGCGCAGCAGTACTGACTCAGATCAGGGGAGACCTTGTCTT 242
 Db 26 LeuLeuGlnAspPheProAlaLeuLeuAsnProGlu----- 37
 QY 243 TTGAGATGATCTCCGACCGCGAGGAGGCGGAT-----TCAGGT 281
 Db 38 ---AspProLeuProTprLysAlaProGlyThrValLeuSerGlnGluValGluGly 56
 QY 282 TCTCTTGCC----- 290
 Db 57 GluLeuAlaGluLeuAlaMetGlyPheLeuGlySerArgLysAlaProProProLeuAla 76
 QY 291 -----ACATCAATATCCGAGATCGTAAAGACTGAA-----GGG 323
 Db 77 AlaAlaLeuAlaHisGluAlaValSerGlnLeuLeuGlnThrAspLeuSerGluPheArg 96
 QY 324 AAGAGCGCAAGAGAAAACTCCGAGGAGAGAGAAAGATGCGACTGAAAGCTTGGCA 383
 Db 97 LysLeuProArgGlnGluGlnGluGlnGlnGlnAspAspArgLysGluGlyAlaPro 116
 QY 384 AAGAAAGTTGTTAAAGCCTCTTCGGTGATCTTTGGTGTGAAGGGCTATGCGCTAGCGG 443
 Db 117 ValThrLeuLeuAspAlaGlnSerLeuValaGlnSerPheAsnArgLeuTrrGluVal 136
 QY 444 AAGGGTGAG----- 452
 Db 137 AlGlyGlnTrrGlnLysGlnValProLeuAlaAlaArgAlaSerGlnArgGlnTrrLeu 156

QY 453 -----AGGAGAGATCGAGATGCCAGCTCATCTG 485
DB 157 ValSerLeuHAlaIleArgAenThrArgArgLeuMetGluNepArgHisValSerLeu 176
QY 486 AACGACATCACCGAGAGGTAGAGCCCCCATCTGCTCATTTACTTGGGTTTCATTTT 545
DB 177 ProSerPhe--AenGluNepPheGlyLeuSerAspProValAsnArg--AlaTyPhe 194
QY 546 GCTGTTTGTATGACATGAGAGATTGCAAGCTCAAAATTGCTGCACAGAAATTGCAT 605
DB 195 AlaValPheAspGlyHisGlyValAlaPheAlaAlaArgTyAlaAlaValHisValHis 214
QY 606 CAAACTTAATACAGAAA-----TTTCTTAAGAGATGTAATCACTGTA 650
DB 215 ThrAsnAlaAlaArgGlnProGluLeuProThrAspProGluGly----- 229
QY 651 GAGAAAACCGTGAAGATGCCCTTTGGACACTTTCAGCATATCTGATGAAGTTCTT 710
DB 230 -----AlaLeuArgGluAlaPheArgArgThrAspGlnMetPheLeu 243
QY 711 AACACAGCTTCACGACGCTGCTGGAAAGATGGGCTCCAGCGTGTCTTG 770
DB 244 ArgGlySerAlaLeuArgGluArg-----LeuGlnSerGlyThrThrGlyValCysAlaLeu 261
QY 771 GCTGTAGACACATCTTTATATTGCGCAACTCGAGATAGTCGGGCAATCTTGTGCT 830
DB 262 IleAlaGlyAlaThrLeuHisValAlaTrpLeuGlyAspSerGlnValIleLeuVal---- 280
QY 831 TTATATGAGAGAGATCAAAACATGACGCTTAAGCTTCAGCAAGAGATTAATCTCACT 890
DB 281 -----GlnGlnGlyValValLeuLeuMetGluTrpHisArgProGlu 295
QY 891 CAGTATGAAGCGGATGAGATACAGAGCTGAGAGAACTGTCAGGAT----- 941
DB 296 ArgGlnAspGlyLeuValArgGlyLeuAlaLeuGlyValPheValSerHisMetAspCys 315
QY 942 GGGCGCTTTTGGCGCTGTAGAGGTGTCACGCTCCATTGGGACCGGACGTAACAAGCC 1001
DB 316 TrpArgValAsnGlyThrLeuAlaValSerArgAlaIleGlyAsp---ValPheGlnLys 334
QY 1002 TGGCGGTACCTCTGTGCGGCATCAACGCTGCACACTGACCCCAATGACAGTTTC 1061
DB 335 ProTyValSerGlyGlyAlaAspAlaAlaSerArgAlaLeuThrGlySerGluAspTyr 354
QY 1062 ATTTGTTGGCTGTGATGGCTCTTCAAGTCTTTAACCCAGAGAGCCGGAATCTTC 1121
DB 355 LeuLeuLeuAlaCysAspGlyPhePheAspValValProHisGlnIleValAlaGlyLeu 374
QY 1122 ATCTGTCTGTCTCGAGATGAAGAATCAAGCCCGGAAAGGAAGTCCGACGCCGAC 1181
DB 375 ValGlnSerHisLeu-----ThrArgGlnGlnGlySerGlyLeuArg 388
QY 1182 GCGCCGCTACGAAGACGCTGCACAGGCTGGCCACAGCGGCTGCGGGCTCGGCC 1241
DB 389 ValAlaGluGln-----LeuValAlaAlaAlaArgGlyArgGlySerHis 403
QY 1242 GACACAGTCACTGTATGGTGGG 1265
DB 404 AspAsnIleThrValMetValVal 411
RESULT 23
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ID AAG18041 standard; Protein; 358 AA.
XX AAG18041;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19292.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR 24-JUN-1999; 99US-0140695.

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PR	26-OCT-1999	99US-0161361
PR	26-OCT-1999	99US-0161362
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PR	28-OCT-1999	99US-0161933
PR	29-OCT-1999	99US-0162142

Alignment Scores:

Pred. No.:

Score:
Percent:

Best Local

Query Match

DB:

ITS-09-935-

88-89

QY 249

ה

DB 15

QY 309

2.

D6 28

369 OY

↓

Db 38

Qy 429

12

Db 42

490

409 57

Pred. No. :	2, 4e-28	Length:	358
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Percent Similarity:	48.13%	Conservative:	54
Best Local Similarity:	33.56%	Mismatch:	102
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US-09-935-124A-1 (1-1422) x AAG18041 (1-358)

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Db	15	AAspMcPProPogLuLyvaLaAspSpGLyLYrTfLe-----	27
OY	309	GTPAAAGACTGAAGGAAAGAGCAAGAAGAAAACTCCGAGAGAAATTGGCAGT	368
Db	28	-----GLyLYvLYrTrPLys-----AAspAspSLySer	37
OY	369	GAAAGAGCTTGAGAAAAAGAAAGTTGTAAAGCCTTCGGGATCTTGGCTGAAGGC	428
Db	38	LauSer-----Cys-----GLy	41
OY	429	TATGTGCTGAGCGGAAGGGTGAAGAGAGATGCAGATGCCACGTATCCTGAAC	488
Db	42	TYCySerSerPheArg-----GLyLysArgSerThMetGluAspPheTyRaspIleLysAla	60
OY	489	GACATCACCGGAGAGTGTTAGGGCCCCCAACGTCGCCCATTAATCTACGGGTTTCATATATTTGCT	548

Db 61 SerThrIleGluGly-----GlnAlaValCysMetPheGly 72
Qy 549 GTTTTGGATGACATGAGAAATTGAGCCTCAAAATTTGTCGACAGATTTCATCA 608
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 73 IlePheArgIleHisGlyIleSerArgAlaGluTyrLeuIleuIleuIleuIleuPhean 92
609 AACTTAATCAGAAATTTCTTAAGAGAGATGTATCATGCTGAGAAAACCTGAAGAGA 668
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 93 AenLeuMet---LysHisProGln-----PheLeuThrArgThrIleu 106
Qy 669 TGGCTTTGGACACTTTCAGACATCTGATGAAAGCTTCTTAAGAACCTTCACGCCG 728
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 107 AlaLeuAenGlnThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 123
Qy 729 AAGCTGCTGAGAAA---GATGGGTCACTGTCACCTGTGTTCTGCTGATGACACATT 785
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 124 LysAspThrTyrArgAspArgSerThrAlaSerAlaValLeuValGlyAsnHis 143
Qy 786 CTTTATATATGCTCAACCTCGAGATAGTCCGAGCAATCTTGTCTGCTTATATAGAGAGT 845
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 144 LeuTyrValAlaAsnValGlyAspSerArgThrIleVal-----Ser 157
Qy 846 CAAAAACATGCAAGCCTTAAGCCTCAAGCAAGACATATCCAACTCATATGAGAGCGG 905
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Db 158 LysAlaGlyLysAlaIleLeuSerAspAspHisLysProAsnArgSerAspGluArg 177
Qy 906 ATGAGGATACAGAGGCTGAGAGAAAGTCAGG-----GATGGCGTGTGTTGGCGC 956
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Db 178 LysArgIleGluSerIleGlyValIleMetThrAlaGlyThrThrArgValGlyGly 197
Qy 957 GTGCTAGAGGTGTACAGCTTCATTTGGGAGACGGGACATACAGGCTTCGCGTGCACCTCT 1016
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Db 198 ValLeuAlaMetSerArgLysPheGlyAsnArgMetLeuIleGlnPhe---ValValAla 216
Qy 1017 GTGCCCGAATACAGAGCTGCCAGCTGACCCCAATGACAGTTCATTTGTGGCTGT 1076
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Db 217 GluProGluIleGlnPheLeuGlnIleAspHisGlnAlaGlnLeuValLeuAlaSer 236
Qy 1077 GATGGGCTTCAAGGCTTTTACCCCAAGAGAGCGCTGAATCTTCCTGTCCTGTC 1136
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Db 237 AspGlyLeuThrAspValValProAsnGlnAspAlaVal-----AlaLeuAlaGlnSer 254
Qy 1137 GAGATGAAAGAATCCAGACCCGGGAGGAGAAAGTCGACGCCGCGCTACGAAGCA 1196
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Db 255 GluGlnGluPro-----GluAla 260
Qy 1197 GGCTGCAAGAGCTGCGCAAGAGGCTGACCGGGGCTCGCGCGACACATGCTGTG 1256
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Db 261 AlaAlaArgLysLeuThrAspThrAlaPheSerArgGlySerAlaAspAsnIleThrCys 280
Qy 1257 ATGTGTGTCGATAGGCAC 1277
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Db 281 IleValValLysPheArgHis 287
RESULT 24
AAG39776
ID AAG39776 standard; Protein; 358 AA.
XX AAG39776;
XX AC
DT 18-OCT-2000 (first entry)
XX DE
XX Arabidopsis thaliana protein fragment SEQ ID NO: 49266.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hydridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX OS
XX EPI033405-A2.
XX PN
XX 06-SEP-2000.
PD

XX 25-FEB-2000; 2000EP-0301439.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

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APPLICANT: Xu, Weiduan  
APPLICANT: Bogenberger, Jakob  
TITLE OF INVENTION: Modulators of Angiogenesis  
FILE REFERENCE: 021044-000210us  
CURRENT APPLICATION NUMBER: US/09/935,124A  
PRIOR FILING DATE: 2002-05-21  
PRIORITY APPLICATION NUMBER: 60/284,760  
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QY 522 CTCAATTAATCTGGGATTCATATATTTGCTGTTTGTATGATGACATGAGAAATTCAGCCTCA 581
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Db 141 LeuIleThrArgValSerThrPheAlaValPheAspGlyHisGlyGlyLysIleArgAlaSer 160
QY 582 AAATTTGGCTGCACAGAAATTTGCATCAAACTTAATCAGAAAATTTCTTAAGAGAGATGTA 641
   |||||
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheSerGlyAspVal 180
QY 642 ATCAGGTGAGAGAAACCGTGAAGAGATGCTTTTGGACATTTCAAGATCTGATGTA 701
   |||||
Db 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGln 200
QY 702 GAGTTCCTTAAACAAGCTTCCAGCAGAGCCTGCTGGAAGATGGGTCCATGCTCCACG 761
   |||||
Db 201 GluPheLeuLysGlnLysSerSerGlnLysProAlaIleTrpLysAspGlySerThrAlaThr 220
QY 762 TGTGTTCTGGCTGTAGACAACATTTCTTAATATGTCACCTCGAGATAGTGGGCAATC 821
   |||||
Db 221 CysValIleValAlaAspAsnIleLeuLysIleAlaAsnLeuGlyAspSerArgAlaIle 240
QY 822 TTGTGTCCTTAATGAAGAGAGAGTCAAAAACATGCAGCCTTAAAGCTTCAGCAAAAGACT 881
   |||||
Db 241 LeuCysArgLysAsnGlnLysSerGlnLysHisAlaAlaLeuSerLeuSerLysGlnLys 260
QY 882 AATCAACTCAGTATGAAGAGCGATGAGATGACAGAAAGCTGAGAGAAACGTCAAGGAT 941
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Db 261 AsnProThrGlnLysGlnLysArgMetArgLysGlnLysAlaGlyLysValAsnValArgAsp 280
QY 942 GGGCGTGTGTTGGCGGTGTAGAGGTGTACGCTTCATTTGGGAGCGGAGCATCAACGCGC 1001
   |||||
Db 281 GlyArgValLeuGlyValLeuGlnValSerArgSerIleGlyAspGlyLysLysArg 300
QY 1002 TGGCGGTGTCACCTGTGTGGCCGACATCAGACGCTGACAGCTGACCCCAATGACAGTTTC 1061
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Db 301 CysGlyValThrThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320

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QY 1062 ATTTGTGGCTGTGATGGGCTTTCAAGGTCTTTACCCAGAGAACCGGTGAATCTTC 1121
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Db 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGlnGlnAlaValAsnPhe 340
QY 1122 ATCTTGTCTGTCTGTGAGAGATGAAGAAATCCAGACCCGGGAAAGGAAATCGCACCCGAC 1181
   |||||
Db 341 IleLeuSerCysLeuGlnAspGlnLysIleGlnThrArgGlnGlyLysSerAlaIleAsp 360
QY 1182 GCCCGCTACGAAGCAGCTGTGCAACAGCTGGCCCAACAGAGCGGTGACAGGGGCTCGGCC 1241
   |||||
Db 361 AlaArgLysGlnAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380
QY 1242 GACAACTCAGTGTGATGATGGTGGTGGATAGGGCAC 1277
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Db 381 AspAsnValThrValMetValValArgLysIleGlyHis 392

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RESULT 2

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US-09-860-351-4
; Sequence 4, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

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Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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US-09-935-124A-1 (1-1422) x US-09-860-351-4 (1-274)

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QY 453 AGGAGAGATGACGAGGCCACGTCATCTGGAACGACATCACGAGAGGTAGGCC 512
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Db 1 ArgLysSerMetGlnAspAlaHisIleAlaLeuLysAsnLeuAsnSerSerSerGly 20
QY 513 CCATGTCCTCATTAATCTCGGGTTTCATATTTGCTGTTTGTATGATGACATGAGAAAT 572
   |||||
Db 21 LysAspSerTrp-----SerPheHeAlaValPheAspGlyHisGlyLys 36
QY 573 CGAGCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTAATC-----AGAAAA 623
   |||||
Db 37 GlnAlaAlaLysTyArgLysGlyLysHisLeuHisLysThrIleLeuAlaGlnLysArgSer 56
QY 624 TTTCCCTAAGAGAT-----GTAACTAGTGAAGAAACCGTGAAGAGA 668
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Db 57 PheProGlnGlnLysAspProTyGlnMetLysLeuSerAspLeuGlnAspAlaLeuLysGlu 76
QY 669 TGCCTTTGACACTTTTCAACATATCTGATGAAGATTTCTTAAACAAGCTTCCAGC--- 725
   |||||
Db 77 SerPheLeuGlnAla-----AspThrAspGlnGlnLysLeuArgSerAlaGlnAlaSerAla 94
QY 726 -----CAGAACCTGCTCGGAAGATGGGTCACTGCGACGCTGTGTTTG 770
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Db 95 AlaAenlyValLeuThrlYsgluAsePLeuSerSerglySerThrlAlValAlaLeu 114
 QY 771 GCTGTAGACAACTTTCTTTATTTGCGCAACTCGAGATAGTCGGCAATCTTGTCGT 830
 Db 115 IleArglyAenlyValAlaAenValIglyAsePserThrgAlaValLeuYsArg 134
 QY 831 TATATAGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAGAGCATATATCAACT 890
 Db 135 ---AenGlyAenAlaIleYsTrp---AlaValThrlLeuThrgluAsePhslySproSer 152
 QY 891 CAGTATGAAAGCGGATGAGATACAGAAAGCGTGAGGA-----AAGCTCAGGAGT 941
 Db 153 AenGluAsePgluAArggluArgIleGluAlaIaglyGlyPheValSerArgValSerAen 172
 QY 942 GGGCGTGTGGGCGTGCATGAGAGTGCACGCTCATTTGGGAGCGGAGTACAG--- 998
 Db 173 GlyAArgValAenGlyValLeuAlaValAseThrgAlaPheGlyAsePhslySpro 192
 QY 999 ---CGCTGCGGT----- 1007
 Db 193 GlySerlyLeuGlyProGluGluSerleuGluAlaAenlyrGluYrIleYsSpro 212
 QY 1008 -----GTCACTCTGTGCGCCGACATC---AGACGCTGCACGCTGACCCCAT--- 1052
 Db 213 GluGluLeuValThrlAlaGluProAsePValThrSerSerThraPLeuThrProAsePly 232
 QY 1053 GACAGGTTCATTTTGTGGCTGTGATGGGCTTTCAGAGTCTTTACCCCAAGAGGCC 1112
 Db 233 AspGluPheLeuIleLeuAlaCyAsePglyLeuThrAsePValValSerAsePgluVal 252
 QY 1113 GTGAACTCATCTGTCTGCTGAGAGTAAAGATCAGACCCGAGAGGAAAGTCC 1172
 Db 253 ValAseP1leValArgSerGluLeuSerAseP-----GlyAenlyS 265
 QY 1173 GCAGCGGAGCCCGCTACGAGAGGCC 1199
 Db 266 SerAlaGluAsePProMetGluAlaAla 274
 RESULT 3
 US-09-828-302-14
 ; Sequence 14, Application US/09828302
 ; Patent No. US20020152502A1
 ; GENERAL INFORMATION
 ; APPLICANT: COSTA E. SILVA, OSWALDO DA
 ; APPLICANT: VAN THIELEN, NOCHA
 ; APPLICANT: CHEN, ROUYING
 ; TITLE OF INVENTION: IN PLANTS
 ; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE
 ; FILE REFERENCE: 16313-0029
 ; CURRENT APPLICATION NUMBER: US/09/828,302
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/196,001
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Physcomitrella patens
 US-09-828-302-14
 Alignment Scores:
 Pred. No.: 3,56e-25 Length: 353
 Score: 375,50 Matches: 109
 Percent Similarity: 43,78% Conservative: 60
 Best Local Similarity: 28,24% Mismatches: 98
 Query Match: 14,67% Indels: 119
 Db: 10 Gaps: 12
 US-09-935-124a-1 (1-1422) x US-09-828-302-14 (1-353)
 QY 339 AAACCTCCGAGAAAGAAAGATGCGAGTGAAGCTTGAGAAAAAGAAAGTTTGTA 398

Db 12 LysThrSerGluAsePArgIuAen----- 19
 QY 399 GCCTCTGGGATGATCTTTGGTGTGAAAGGGCTATGTGGCTGACGGAAAGGTGAGAGAG 458
 Db 20 ---AlaGluAenAArglyrGlyLeu-----SerAlaMetGlnIlyrThrgAseP 34
 QY 459 GAGATGACAGATGCCCGCTCATCCGAAACACATCCAGACCGAGAGTGTAGGCCCATCG 518
 Db 35 SerMetGluAsePAlaHslySalIleAenValAsePlyAseAen----- 49
 QY 519 TCCCTCATCTACGAGTTTCATATTTTGGCTTTTGTGATGACATGAGAGATTCAGACC 578
 Db 50 -----ThrSerThrSerIlePheGlyIlePheAsePglyHslyGlylyValLeuAl 66
 QY 579 TCMAATTTGCTGCACAGAAATTTGCATCAAAACTTAATCAGAAA-----TTTCTTAA 632
 Db 67 AlAlyPheCySalAlyShIleuHslyGlnGluValLeuYsSerGluAlAlyrAlAlyS 86
 QY 633 GAGATGTATACAGTGTAGAGAAAAACGTGAAGAGATGCTTTTGAACACTTTCAGACT 692
 Db 87 GlyAseP-----LeuYsAlaSerleuGluYrSerPheLeuArg 99
 QY 693 ACTGATGAA-----GAGTTCCTTAAACAGCT 719
 Db 100 MetAsePgluMetleuYsGlyAlaSerGlyTrplyGluLeuGlnSerleuGluGluThr 119
 QY 720 TCCAGGCA----- 728
 Db 120 SerSerIleuAsePlyLeuGlyAenGlyAenSerSerSerAenAlAArgIuAseP 139
 QY 728 ----- 728
 Db 140 GluSerAsePlySerTrAlaValLeuThrlGluSerAsePserAenLeuAlaThrlYs 159
 QY 729 AAGCTGCTGGAAGAT-----GGTCCACGCGCACCGTGTTCTG 770
 Db 160 LysHslyAlySerSerAsePheGlnGlyProIleYrGlySerThrlAlaValAlaLeu 179
 QY 771 GCTGTAGACAACTTTTATATTTGCCAACCCTCGAGATAGTCGGCAATCTTGTCGT 830
 Db 180 IleArgglyAenlyValLeuPheValAlaAsePValAsePserAlyrIleMetSerAen 199
 QY 831 TATATGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAGAGCATATTCAACT 890
 Db 200 ArgglyGlu-----AlaValAsePserIleAsePhslySproAse 213
 QY 891 CAGTATGAAAGCGGATGAGATACAGAAAGCTGAGAGAAAGTCAAGGATGGCGTGT 950
 Db 214 LeuGluHslyGluArglyAArgIleGluSerAlaglyPheValHslyGlyAArgVal 233
 QY 951 TTGGCGGTGTAGAGGTGACGCTCCATTTGGGAGACGGCAGTACAG----- 998
 Db 234 AenGlySerleuAsePLeuThrgAlaIleGlyAsePmetGluPheGlyAArgProAse 253
 QY 999 -----CGTGCAGGTGCACCTGTGTCGCGAGCATCAGACGCTGCAGCTGACC 1046
 Db 254 LeuProProAsePlyGluValValThrCyAsePProAsePlyValGluValAsePleuGly 273
 QY 1047 CCCAATGACAGTTCAATTTTGTGGCTGTGAGAGGTCTTCAGGCTTTTACCCCGAA 1106
 Db 274 ProGlyAsePgluPheIleValLeuAlaCyAsePlyIleThrgAsePValMetSerGln 293
 QY 1107 GAAGCGTGAATTCATCTTGCTGTCTGATGAGATAAAGATCCAGACCCGGGAAGG 1166
 Db 294 AlaValAlaAsePheValIlySserArgLeuProThrThryS----- 307
 QY 1167 AAGTCCGAGCGACGCCGCTACAGAGCAGCTGCAACAGGCTGGCCCAACAGCGGTG 1226
 Db 308 -----ThrLeuSerleuYsGluGluIleLeuAsePlyrCyLeu 321
 QY 1227 -----CAGCGGGGCTCGGCGCAGCAAGCTCATGTGATGTGTGTCGAGTA 1271

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Db 322 SerProthThrArgInglIngluGlyCyAspAsnMetSerIleIleValGlnPro 341
Qy 1272 GGGCACTGAGGGGTGGCG 1289
Db 342 LysGlnSerGlyValAla 347

RESULT 4
US-10-178-977A-2
; Sequence 2, Application US/10178977A
; Publication No. US20030014776A1
; GENERAL INFORMATION:
; APPLICANT: University of Zurich
; APPLICANT: Cold Spring Harbor Laboratory
; APPLICANT: Grossniklaus, Ueli
; APPLICANT: Huck, No. US20030014776A1bert
; APPLICANT: Moore, James M.
; TITLE OF INVENTION: MATERNAL EFFECT GAMETOPHYTE REGULATORY POLYNUCLEOTIDE
; FILE REFERENCE: feironia
; CURRENT APPLICATION NUMBER: US/10/178,977A
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/300,624
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-178-977A-2

Alignment Scores:
Pred. No.: 1,14e-23 Length: 361
Score: 358.50 Matches: 86
Percent Similarity: 51.25% Conservative: 58
Best Local Similarity: 30.60% Mismatches: 96
Query Match: 14.00% Indels: 41
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-10-178-977A-2 (1-361)
Qy 444 AAGGGTGAAGGAGAGAGATGCGAGATGCCCATCTCTGAAGCATCCAGGAG 503
Db 79 LysGlyProLysGlnSerMetGlnAspGlnPheIleCysValAspAsnLeuThrGlnTyr 98
Qy 504 TGTAGGCCCCCATCGTCCCTCACTTACTCGGGTTTCATATTTCGCTTTTGTGAGCAT 563
Db 99 IleGlySerSerThrGly-----AlaPheTyrGlyValIlePheAspGlnHis 113
Qy 564 GGAGGAATTCGAGCTCAAAATTTGCTGCACAGAAATTCGATCAAAATTAATC----- 617
Db 114 GlyGlyValAspAlaSerPheThrLysLysAsnIleMetLysLeuValMetGlnAsp 133
Qy 618 AAAAAATTTCCATAAGGAGATGTAATCAGTGAAGAAAACGCTGAAGAGATCCCTTTTG 677
Db 134 LysHisPhePro-----ThSerThrLysLysAlaThrArg 145
Qy 678 GACACTTTCAAGCATAGTATGAGAGATTCTTAAACAAGCTTCCAGCAGAGCTGGCC 737
Db 146 SerAlaPheValLysThrAspHisAlaLeuAlaAspAlaSerSerLeuAspArg----- 163
Qy 738 TGGAAAGATGGGTCCACTGCCACGTGTGTTCTGGCTGAGACAACATTTCTTATATGGC 797
Db 164 ---SerSerGlyThrThrLysAlaLeuThrAlaLeuIleLeuAspLysThrMetLeuIleAla 182
Qy 798 AACCTCGGAGATAGTCGGGCAATCTTGTCGTATTATAGAGAGAGTCAAAAACATGCA 857
Db 183 AsnAlaGlyLysSerArgAlaValLeu-----GlyLysArgGlyArg 196
Qy 858 GCCTTAAGCTCGCAAAAGCATTAATCCAACTCAGTATGAGAGAGAGATGAGATACAG 917
Db 197 AlaIleGlnLeuSerLysAspHisLysProAsnCysThrSerGlnArgLeuArgIleGln 216
Qy 918 AAGCTGAGGAAACGTCAGGAGATGGCGTGTGTTGGCGTGTAGAGGTGTCAAGCTCC 977
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Db 217 LysLeuGlnGlyValIleTyrAspGlyTyrLysAsnGlnLysLeuSerValAlaArgAla 236
Qy 978 ATTGGGAGCGGAGCAGTACAG-----CCGTGGGAGTGCAGCTCTGTGCCC 1022
Db 237 LeuGlyAspThrPheIleLysGlyThrLysGlySerLeuCysProLeuSerCysGlnPro 256
Qy 1023 GACATCAAGCGCTGCCAGCTGACCCCAATGACAGGTTCAATTTGTGGCTGTGATGGG 1082
Db 257 GlnLeuGlnGlnIleValLeuThrGlnGlnAspGlnTyrLeuIleMetGlyCysAspGly 276
Qy 1083 CTTTCAAGTCTTTTATCCCCAGAGAACCCGCGAATTCATCTTCTCTGTCCAGAGAT 1142
Db 277 LeuTrpAspValMetSerSerGlnCysAlaValThrMetVal-----ArgArg 292
Qy 1143 GAAAGATTCAGACCCGGGAGGAGGATCCGACGCCGCGCTTACGAGACAGCAGCTGC 1202
Db 293 GlnLeuMetGlnHisAsnAspProGlnArgCysSerGlnAla----- 306
Qy 1203 AACAGCTTGGCCCAAGCAGCGGTGACGCGGAGCTGCGCCGACCACTGATGATGG 1262
Db 307 -----LeuValLysGlnAlaLeuGlnIleArgAsnSerCysAspAsnLeuThrValVal 324
Qy 1263 GTG 1265
Db 325 Val 325

RESULT 5
US-10-178-977A-4
; Sequence 4, Application US/10178977A
; Publication No. US20030014776A1
; GENERAL INFORMATION:
; APPLICANT: University of Zurich
; APPLICANT: Cold Spring Harbor Laboratory
; APPLICANT: Grossniklaus, Ueli
; APPLICANT: Huck, No. US20030014776A1bert
; APPLICANT: Moore, James M.
; TITLE OF INVENTION: MATERNAL EFFECT GAMETOPHYTE REGULATORY POLYNUCLEOTIDE
; FILE REFERENCE: feironia
; CURRENT APPLICATION NUMBER: US/10/178,977A
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/300,624
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-178-977A-4

Alignment Scores:
Pred. No.: 1,14e-23 Length: 361
Score: 358.50 Matches: 86
Percent Similarity: 51.25% Conservative: 58
Best Local Similarity: 30.60% Mismatches: 96
Query Match: 14.00% Indels: 41
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-10-178-977A-4 (1-361)
Qy 444 AAGGGTGAAGGAGAGAGATGCGAGATGCCCATCTCTGAAGCATCCAGGAG 503
Db 79 LysGlyProLysGlnSerMetGlnAspGlnPheIleCysValAspAsnLeuThrGlnTyr 98
Qy 504 TGTAGGCCCCCATCGTCCCTCACTTACTCGGGTTTCATATTTCGCTTTTGTGAGCAT 563
Db 99 IleGlySerSerThrGly-----AlaPheTyrGlyValIlePheAspGlnHis 113
Qy 564 GGAGGAATTCGAGCTCAAAATTTGCTGCACAGAAATTCGATCAAAATTAATC----- 617
Db 114 GlyGlyValAspAlaSerPheThrLysLysAsnIleMetLysLeuValMetGlnAsp 133
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Qy 618 AGAAATTTCTTAAGAGATGTAATCACTGATGAGAAAACCTGAGAGATGCTTTG 677
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Db 134 LysHisPhePro-----ThrsThrLysLysAlaThrArg 145
Qy 678 GACACTTTCAGACATCTGATGAGAGTTCTTAAACAGCTTCAGCCGAGAACCTGCC 737
   |||
   |||
   |||
Db 146 SerAlaPheValLysThrAspHisAlaLeuAlaAspAlaSerSerLeuAspArg----- 163
Qy 738 TGGAAAGATGGGTCCACTGCGACGTGTGTGCTGTGATGACAAATCTTTATATTGCC 797
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   |||
Db 164 ---SerSerGlyThrThrAlaLeuThrAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAla 182
Qy 798 AACCTCGAGATAGTCGGGCGCATCTGTGCTGCTTATATAGAGAGATCAAAACATGCA 857
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Db 183 AsnAlaGlyAspSerAspAlaValLeu-----GlyLysArgGlyArg 196
Qy 858 GCCTTAAGCTTCAGAAAGAGCATTAATCCAGTATGAGAGCGGATGAGATACAG 917
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Db 197 AlalGluLeuSerLysAspHisLysProAsnCyThrSerGluArgLeuAlaGlyLeu 216
Qy 918 AAGCTGAGGAAAGCTCAGAGATGGCGCTGTTGGCGCTGATGAGGTGTCAGCTCC 977
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Db 217 LysLeuGlyGlyValIleTyrAspGlyTyrLeuAsnGlyGlnLeuSerValAlaArgAla 236
Qy 978 ATGGGGACGGGACGTACAG-----CGCTGCGGTGCACCTCTGTGCC 1022
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Db 237 LeuGlyAspTyrPheHisIleLysGlyThrLysGlySerLeuCyProLeuSerCyGluPro 256
Qy 1023 GACATCAGACGCTGCGACGTGACCCCAATGACAGGTTCAATTTGTGGCTGTATGG 1082
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   |||
   |||
Db 257 GluLeuGluGluIleValLeuThrGluGluAspGluTyrLeuIleMetGlyCyAspGly 276
Qy 1083 CTCTTCAGAGCTTTTACCCCAAGAGAACCGGTGAACCTTCATCTGTCTCGAGGAT 1142
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Db 277 LeuTyrAspValMetSerSerGlnCyAlaValThrMetVal-----ArgArg 292
Qy 1143 GAAAGATCCAGACCCGGGAGAGAGTCGACGACCGCCGCTTACAGACGCTGC 1202
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   |||
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Db 293 GluLeuMetGlnHisAsnAspProGluArgCySerGlnAla----- 306
Qy 1203 AACAGCTGGCCAAACAGCGGTGACGAGGGCTCGCGCAGACAGATGATGATG 1262
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Db 307 -----LeuValLysGluLysAlaLeuGlnArgAsnSerCyAspAsnLeuThrValVal 324
Qy 1263 GTG 1265
Db 325 Val 325

RESULT 6
US-10-178-977A-6
; Sequence 6, Application US/10178977A
; Publication No. US20030014776A1
; GENERAL INFORMATION:
; APPLICANT: University of Zurich
; APPLICANT: Cold Spring Harbor Laboratory
; APPLICANT: Grosniklaus, Ueli
; APPLICANT: Huck, No. US20030014776A1bert
; APPLICANT: Moore, James M.
; TITLE OF INVENTION: MATERNAL EFFECT GAMETOPHYTE REGULATORY POLYNUCLEOTIDE
; FILE REFERENCE: Ieronia
; CURRENT APPLICATION NUMBER: US/10/178, 977A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/300,624
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-178-977A-6

Alignment Scores:

Pred. No.: 1,14e-23 Length: 361
Score: 358.50 Matches: 86
Percent Similarity: 51.25% Conservative: 58
Best local Similarity: 30.60% Mismatches: 96
Query Match: 14.00% Indels: 41
DB: 9 Gaps: 8

US-09-935-124A-1 (1-1422) x US-10-178-977A-6 (1-361)
Qy 444 AAGGTGAGAGAGAGAGAGATGCGAGATGCGCACGTCATCTCGAAGCATCAACGAGAG 503
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Db 79 LysGlyProLysGlnSerMetGluAspGluPheIleCyValAspAspLeuThrGluThr 98
Qy 504 TGTAGCCCCCATGCTCCATTAATCTCGGTTTCAATTTGTGCTTTTGTGATGAGACT 563
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   |||
   |||
Db 99 IleGlySerSerThrGly-----AlaPheTyrGlyValIlePheAspGlyHis 113
Qy 564 GAGGAAATTCAGACCTCAAAATTTGCTGCAAGAAATTTGCATCAAAACTTAATC----- 617
   |||
   |||
   |||
Db 114 GlyGlyValAlaAspAlaAspPheThrLysAsnIleMetLysLeuValMetGluAsp 133
Qy 618 AGAAATTTCTTAAGAGATGTAATCACTGATGAGAAAACCTGAGAGATGCTTTTG 677
   |||
   |||
   |||
Db 134 LysHisPhePro-----ThrsThrLysLysAlaThrArg 145
Qy 678 GACACTTTCAGACATCTGATGAGAGTTCTTAAACAGCTTCAGCCGAGAACCTGCC 737
   |||
   |||
   |||
Db 146 SerAlaPheValLysThrAspHisAlaLeuAlaAspAlaSerSerLeuAspArg----- 163
Qy 738 TGGAAAGATGGGTCCACTGCGACGTGTGTGCTGTGATGACAAATCTTTATATTGCC 797
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Db 164 ---SerSerGlyThrThrAlaLeuThrAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAla 182
Qy 798 AACCTCGAGATAGTCGGGCGCATCTGTGCTGCTTATATAGAGAGATCAAAACATGCA 857
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   |||
   |||
Db 183 AsnAlaGlyAspSerAspAlaValLeu-----GlyLysArgGlyArg 196
Qy 858 GCCTTAAGCTTCAGAAAGAGCATTAATCCAGTATGAGAGCGGATGAGATACAG 917
   |||
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   |||
Db 197 AlalGluLeuSerLysAspHisLysProAsnCyThrSerGluArgLeuAlaGlyLeu 216
Qy 918 AAGCTGAGGAAAGCTCAGAGATGGCGCTGTTGGCGCTGATGAGGTGTCAGCTCC 977
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   |||
   |||
Db 217 LysLeuGlyGlyValIleTyrAspGlyTyrLeuAsnGlyGlnLeuSerValAlaArgAla 236
Qy 978 ATGGGGACGGGACGTACAG-----CGCTGCGGTGCACCTCTGTGCC 1022
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Db 237 LeuGlyAspTyrPheHisIleLysGlyThrLysGlySerLeuCyProLeuSerCyGluPro 256
Qy 1023 GACATCAGACGCTGCGACGTGACCCCAATGACAGGTTCAATTTGTGGCTGTATGG 1082
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Db 257 GluLeuGluGluIleValLeuThrGluGluAspGluTyrLeuIleMetGlyCyAspGly 276
Qy 1083 CTCTTCAGAGCTTTTACCCCAAGAGAACCGGTGAACCTTCATCTGTCTCGAGGAT 1142
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   |||
Db 277 LeuTyrAspValMetSerSerGlnCyAlaValThrMetVal-----ArgArg 292
Qy 1143 GAAAGATCCAGACCCGGGAGAGAGTCGACGACCGCCGCTTACAGACGCTGC 1202
   |||
   |||
   |||
Db 293 GluLeuMetGlnHisAsnAspProGluArgCySerGlnAla----- 306
Qy 1203 AACAGCTGGCCAAACAGCGGTGACGAGGGCTCGCGCAGACAGATGATGATG 1262
   |||
   |||
   |||
Db 307 -----LeuValLysGluLysAlaLeuGlnArgAsnSerCyAspAsnLeuThrValVal 324
Qy 1263 GTG 1265
Db 325 Val 325

RESULT 7
US-09-972-741-2
; Sequence 2, Application US/09972741
; Patent No. US2002010070A1

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DB: 9 Gaps: 9
US-09-935-124A-1 (1-1422) x US-10-072-130-3 (1-390)
QY 333 AAGAGAAAACTCCGAGAGAGAGAGATGGCAAGAGCTTGTGGAAAAAGATT 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 LysProLysThrGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
QY 393 TGTAAAGCTCTTCGGTGAATCTTGTGTGTGAAGGGTATGTGGCTGAGCGGAAGGTGAG 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyr 32
QY 453 AGGAGAGATGACAGATGCGCAGCATGCTGAGACAGACACGAGAGAGTAAAGCCC 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 ArgValGluMetGluAspAlaHisThrAlaValAlaGlyIle----- 46
QY 513 CCAATGCTCTGATTAATCTCGGGTTTCAATATTTGCTGTTTGTGATGACATGAGGAAATT 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 ProHisGlyLeu---GluAspTyrSerPhePheAlaValTyrAspGlyHisAlaGlySer 65
QY 573 CAGAGCTCAAAATTTGCTGACAGAAATTTGCATCAAAAGCTA-----ATC 617
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 ArgValAlaAsnTyrCysSerThrHisLeuLeuGlnHisIleThrHisGluAspPhe 85
QY 618 AGAAATTTCTTAAGAGATGTAATC-----AGTTGAGAAAAACCTGAAAGACA 668
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ArgAlaAlaAspLysSerGlyPheAlaLeuGluProSerValGlu---AsnValLysThr 104
QY 669 TGCCTTTGGACACTTTCAGACATATGATGAGAGAGTTCTTAAACAAGCTTCCAGCCAG 728
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 GlyIleArgThrGlyPheLeuLysIleAspGlyTyrMetArgAsnPheSerAspLeuArg 124
QY 729 AAGCTGCTGGAAAGATGGGTCCATGCGCAGCTGTGTTGCTGTGATGACAAATTCTT 788
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 AsnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetIleSerProThrHisIle 144
QY 789 TATATGGCAACCTCGAGATAGTCGGGCAATCTTGTGCTTATATGAGAGATCA 848
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 TyrPheIleAsnGlyAspSerGlyAlaValLeuCysArgAsnGlyGln----- 161
QY 849 AAACATGCAAGCTTAAGCTCAAGAAAGACATTAATCAATCAAGTAAAGAGCGGATG 908
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 -----ValCysPheSerThrGlnAspHisLeuProCysAsnProMetGluLysGlu 178
QY 909 AGGATCAAGAGGCTGAGAGAAACGTGAGGATGGCGGCTTTGGCGGCTTAAGAGT 968
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
QY 969 TCACGCTCCATTTGGGAGAGCGGCACTACAAAGCGCTCGGCT----- 1007
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Db 199 SerArgAlaLeuGlyAspTyrAspTyrLysCysValAspGlyLysGlyProThrGluGln 218
QY 1008 --GTCACCTGTGTCCCGACATCAAGACGCTGCGACGCTGACCCCAATGACAGGTTCAAT 1064
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 LeuValSerProGluProGluValTyrGluIleLeuArgAlaGluGluAspGluPheVal 238
QY 1065 TTGTGGCTGTGATGAGGCTCTTCAGGTTTATCCCGAGAGAGAGCGGTAATTCATC 1124
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Db 239 ValLeuAlaCysAspGlyIleTyrAspValMetSerAsnGlnGluLeuCysGlyPheVal 258
QY 1125 TTGTCTGTCTGAGATGAAAGATCAAGACCCGGGAGAGGAGAGTCCGACGCGCGCC 1184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 AsnSerArgLeuGly-----ValSerAsp 266
QY 1185 CGGTACAGAGAGCTGCAAGAGCTGCGCAAGAGCGGATGACAGGAGGCTGCGCGCAC 1244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AspLeuGluAsnValCysAsnTyrValValAspThrCysLeuHisLeuGlySerAspArg 286
QY 1245 AACGTCACTGATGATGATG 1265
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Db 287 AsnMetSerIleValLeuVal 293
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RESULT 9

US-09-801-368-278
/ Sequence 278, Application US/09801368
/ Patent No. US20020128250A1
/ GENERAL INFORMATION:
/ APPLICANT: Bueby, Robert
/ APPLICANT: Call, Brian
/ APPLICANT: Hecht, Peter
/ APPLICANT: Holzman, Doug
/ APPLICANT: Madden, Kevin
/ APPLICANT: Maxon, Mary
/ APPLICANT: Milne, Todd
/ APPLICANT: No. US20020128250A1man, Thea
/ APPLICANT: Royer, John
/ APPLICANT: Salama, Sofie
/ APPLICANT: Sherman, Amir
/ APPLICANT: Silva, Jeff
/ APPLICANT: Summers, Eric
/ TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
/ FILE REFERENCES: 109272.147
/ CURRENT APPLICATION NUMBER: US/09/801,368
/ PRIOR FILING DATE: 2001-03-07
/ PRIOR APPLICATION NUMBER: US 09/487,558
/ PRIOR FILING DATE: 2000-01-19
/ PRIOR APPLICATION NUMBER: US 60/160,587
/ NUMBER OF SEQ ID NOS: 440
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 278
/ LENGTH: 281
/ TYPE: PRF
/ ORGANISM: Saccharomyces cerevisiae
US-09-801-368-278

Alignment Scores:
Pred. No.: 4,296-20 Length: 281
Score: 317.50 Matches: 95
Percent Similarity: 45.87% Conservative: 44
Best Local Similarity: 31.35% Mismatches: 93
Query Match: 12.40% Indels: 71
DB: 10 Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-801-368-278 (1-281)
QY 432 GTGGCTGAGCGGAGAGGTGAG-----AGGAGAGATGAGATGCCAGTATCCTG 485
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Db 23 ValHisGluAsnLysAsnSerLysPheArgThrMetCysAspValHisThrTyrVal 42
QY 486 AACGACATCACGAGAGAGTGAAGCCCATCGTCCCTCATTAATCTGGGTT-----TCA 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 LysAsnPheAla-----SerArgLeuAspTyrGly 52
QY 540 TATTTGCTGTGTTGATGACATGAGAAATTCAGACTCAAAATTTGCTGACAGAT 599
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 TyrPheHisValPheAspGlyHisAlaGlyIleGlnHisSerLysTyrCysGlyLysHis 72
QY 600 TTGCAT-----CAAACTTAATCAGAAATTTCTTAAGAGATGTAATCACT 647
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 LeuHisThrIleIleGlnGlnAsnIleLeu-----AlaAsp 84
QY 648 GTAGAGAAACCGTGAAGATGCTTTTGGACATTTCAAGCATATGATGAAGATTC 707
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 GluThrArgAspValArgAspValLeuAsnAspSerPheLeuAlaIleAspGluIle 104
QY 708 CTTAAACAAGCTTCCAGCGAGAGCTGCTGGAAGATGGGTCACCT---GCCAGCTGT 764
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 -----AsnThrLysLeuValGlyLysSerGlyCysThrAlaAlaValCys 119
QY 765 GTTCTG-----GCTGTAGCAACAT----- 785
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Db 120 ValLeuArgTyrProLysLeuProAspSerValSerAspAspSerMetAspLeuAlaGlnHis 139
QY 786 -----CTTATATTTGCGCAAGCTGCGAGATGATGCTGCGGCAATCTGTGCTTAATAT 836
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 140 GlnArgLysLeuThrThrAlaAsnValGlyAspSerArgIleValLeuPheArgAsnGly 159
Qy 837 GAGGAGAGTCAAAAATCATCAGCCTTAAGCCTTCAGCAAGAGCATTAATCAATCAGTAT 896
Db 160 Aaa-----serLeaArgLeuThrTyrAspHisbLysAlaSerAspThr 173
Qy 897 GAAGACCGGATGAGTATACAGAAAGCTGAGAGAAACGTACAGGATGGGCTGTTTGGGC 956
Db 174 LeuGluMetGlnArgValGluGlnAlaGlyLeuIleMetLysSerArgValAsnGly 193
Qy 957 GAGTACAGAGTGCACAGCTGAGCGGAGCGGAGCATACAGCGCTGCGGTGACCTCT 1016
Db 194 MetLeuAlaValThrArgSerLeuGlyAspLysPhePheAspSerLeuValAlaGlySer 213
Qy 1017 GTGCCGACATCAGACGCTGACCGCATGACCCCAATGACAGGTTCAATTTGTGGCCTGT 1076
Db 214 ---ProPheThrThrSerValGluIleThrSerGluAspLysPheLeuIleLeuAlaCys 232
Qy 1077 GATGGGCTTTTCAAGTCTTTTACCAGCAAGCGGTGACAGCGGTAACTTCACTTGTCTGTCTC 1136
Db 233 AspGlyLeuThrAspValIleAspAspGlnAspAlaCysGluLeuIleLysAspIleThr 252
Qy 1117 GAGGATGAAAAGATCCAGACCCGGGAAGGAAAGTCCGACCGCAGCCCGCTACAGAGA 1196
Db 253 GluProAsnGlu----- 256
Qy 1197 GCCTGCACAGCGCTGCGCAACAGCGGTGACAGCGGCTCGCGCCAGACAGTCACTGTG 1256
Db 257 AlaAlaLysValLeuValArgTyrAlaLeuGluAsnGlyThrThrAspAsnValThrVal 276
Qy 1257 ATGGTGGTG 1265
Db 277 MetValVal 279
RESULT 10
US-09-973-941-4
Sequence 4, Application US/09973941
Patent No. US2002016465A1
GENERAL INFORMATION:
APPLICANT: Roche, Jean-Marc
APPLICANT: Roche, Paul L.
APPLICANT: Helchman, Karen
TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
TITLE OF INVENTION: Diseases
FILE REFERENCE: Protein Interactions in ND
CURRENT APPLICATION NUMBER: US/09/973,941
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/240,790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: US 60/304,775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
US-09-973-941-4
Alignment Scores:
Pred. No.: 5.38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.33% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
DB: 9 Gaps: 15
US-09-935-124A-1 (1-1422) x US-09-973-941-4 (1-372)
Qy 180 CTGCCTTTTGATGAC-----CTCCCTCCGGCCAGAGACTGACTCA----- 221
Db 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46

Qy 222 -----GGATCAGGGGACCTTTGTTTGATGAT----- 251
Db 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnGlyIle 66
Qy 252 -----CTCCACCCCGCTAGACAGTGGCATTCAGGT 281
Db 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
Qy 282 TCTCTGGCACATCAATATCCAGATGTAAAGACTGAAGGAAAGAGACAAAGAGAAA 341
Db 81 ----- 81
Qy 342 ACCTCCGAGAGAGAGAAATGACGTAGAAGCTTTGAAAAGAAATTGTAAGCC 401
Db 82 -----LysTyrGly-----LysProIleProLysIle 90
Qy 402 TCTTCGGTGAATTTTGTGTGTAAGGCTATGTGCTGAGCGGAGAGGATGAGAGAGAG 461
Db 91 SerLeuGluAsnValGlyCysAlaSerGlnIleGlyLysArgLys--GluAsnGluAsp 109
Qy 462 ATGCAGATGCCACGTCATCCTGAACGACATCACCGAGAGGTGAGGCCCATGTCC 521
Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
Qy 522 CTGATTAAGTCCGGTTTCATATTTTGTCTGTTTGAATGACATGAGAAATTCAGACCTCA 581
Db 120 -----ValLeuTyrPheAlaValIleGlyAspGlnIleGlyProAlaAlaIle 135
Qy 582 AAATTGCTGCACAGAAATTTGATCAAAAATTATCAAGAAATTTCTTAAAGAGATGA 641
Db 136 AspPheCysHisThrHisMetGlnLysCysIleMetAspLeuProLys----- 152
Qy 642 ATCAGTGTAGAGAAAACCGTAAGAGATGCTTTTGAGACATTTCAGACATTAAGTGA 701
Db 153 -----GluLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGluIleAspLys 169
Qy 702 GAGTTCCTTAAACAGCT-----TCAGCCAGAAAGCTGCTGAAAGATGGTCACT 755
Db 170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuThrSerGlyThrThr 189
Qy 756 GCCACGTGTGTTGCTGCTGTGACAACTT--CTTTATTTGCTCCAACTGGAGATAGT 812
Db 190 AlaThrValAlaLeuLeuAspArgAspIleGluLeuValAlaHisSerValGlyAspSer 209
Qy 813 CGGGCAATCTTGTCGTTATATGAGAGAGTCAAAAACATGACCTTAAAGCTCAGC 872
Db 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetLysLeuThr 223
Qy 873 AAAGAGCATTAATCCAACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAGA--- 929
Db 224 IleAspHisThrProGluArgLysAspGlnLysGlnIleLysLysCysGlyGlyPhe 243
Qy 930 -----AACGTACGAGATGGCGCTGTTTGGCGCTGTAAGAGTGCACGCTCC 977
Db 244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
Qy 978 ATTGGGAGCGGACAGTACAAAGCGCTGCGTCACTCTGTGCGGACATCAGACGCTGC 1037
Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGlnThrLysArgIle 283
Qy 1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTGGCTGTGATGGCTTTCAAGGTC 1094
Db 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
Qy 1095 TTTACCCCAAGAAAGCGGTGAATTCATCTTTGCTGTCTGACAGATGAAAAGATCCAG 1154
Db 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
Qy 1155 ACCCGGAAGGGAAGTCCGCGACCGACGCCCGCTACGAAAGACGCTGAAACAGCGTGC 1214
Db 322 -----AlaAlaHisAlaValThr 327
Qy 1215 AACAAAGCGGTGACAGCGGCTCGCGCAACAGTCACTGTGATGTTGTTGCGATAGGG 1274

342 ACCTCCGAGAAAGAGTGGCAGTGAAGAGCTTGGAAAAAGAAAGTTGTTAAAGCC 401
 Db -----LysTyrGly-----LysProIleProLysIle 90
 82 -----LysTyrGly-----LysProIleProLysIle 90
 402 TCTTCGGTATCTTTGGCTGGAAGGGCTATGGCTGAGCGGAAGGGTGAAGGAGAG 461
 Db 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgLys-----GluAsnGluAsp 109
 462 ATGCAGATGCCACGTCATCTCTGAAGACATCCAGGAGAGTGAAGGCCCATGCTCC 521
 Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
 522 CTCATTACTCGGGTTTCATATTTTGTCTTTTATGATGACATGAGCAATCGAGCTCA 581
 Db 120 -----ValLeuTyrPheAlaValTyrAspGlyAsnGlyGlyProAlaAlaAla 135
 582 AAATTTGTCACAGAAATTTGCATCAAAATTATCAAGAAATTTCTTAAGAGATGTA 641
 Db 136 AspPheCysuHsIleThiIleMetGluLysCysIleMetAspLeuPheProLys----- 152
 642 ATCAAGTGTAGAAAACCGTGAAGAGATGCTTTTGGACATTTCAAGCATACTATGA 701
 Db 153 -----GluLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGlnIleAspLys 169
 702 GAGTTCCTTAACAAGCT-----TCCAGCCAGAAAGCTCCTGGAAAGATGGGCTCACT 755
 Db 170 AlaPheSerSerHsAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
 756 GCCACGTGTCTGTGCTGTAGACAACTT-----CTTATATTTGCCACCTCGAGATAGT 812
 Db 190 AlaThrValAlaLeuLeuAspArgLysIleGluLeuValAlaIleSerValGlyAspSer 209
 813 CGGCAATCTGTGTGCTTATATGAGAGAGATCAAAACATGACGCTTAAGCTCCAG 872
 Db 210 ArgAlaIleuLysArgLys-----LysGlyLysProMetLysLeuThr 223
 873 AAAGAGCATTAATCAACTCAGATGTAAGAAAGCGATGATACAGAGCTGAGAGA-- 929
 Db 224 IleAspHisThrProGlnLysAspLeuLysLeuArgLysIleLysLysCysGlyGlyPhe 243
 930 -----AACCTCAGGAGATGGCGGCTTTTGGCGCTGCTAGAGTCAAGCTGCC 977
 Db 244 ValAlaThrAsnSerLeuLysLysProHisValAsnGlyArgLeuAlaMetThrArgSer 263
 978 ATTGGGAGCGGAGATCAAGAGCGCTGCGAGTCACTCTGTGCGGACATCAAGCGCTGC 1037
 Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGlnProGlnThrLysArgIle 283
 1038 CAGCTG--ACCCCACTGACAGAGTTCAATTTTGTGCGCTGTGATGGCTCTTCAAGCTC 1094
 Db 284 LysLeuHisValAspAspSerPheLeuValLeuThrThaAspGlyIleAsnPheMet 303
 1095 TTTTACCACAGAAAGACCGTGAATCTTGTCTGTCTGTCTGACATGAGAAAGATCCAG 1154
 Db 304 ValAsnSerGlnIleLysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
 1155 ACCGGGAAAGAAAGTCCGAGCGCAGCCCGCTACAGAAAGACCGTCAAGAGCTGAGCC 1214
 Db 322 -----AlaIleHisValAlaThr 327
 1215 AAACAAGCGGTGACAGCGGGGCTCGCGCACAAGCTCATGTGATGTGGTGGATGAGG 1274
 Db 328 GluGlnAlaIleGlnIleLysLysThrGluAspAsnSerThrAlaValAlaValProPheLys 347
 1275 CACTGAGGGGCGGCGCGCCAGGAG 1301
 Db 348 AlaThrGlyLysTyrLysAsnSerGln 356

RESULT 14
 US-09-973-063-4
 / Sequence 4, Application US/09973063
 / Patent No. US20020115119A1
 / GENERAL INFORMATION:

APPLICANT: Koch, Jean-Marc
 APPLICANT: Bartel, Paul L.
 TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
 FILE REFERENCE: Diseases
 CURRENT FILING DATE: 2001-10-10
 PRIOR FILING DATE: 2000-10-17
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4
 LENGTH: 372
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-973-063-4

Alignment Scores:
 Pred. No.: 5,38e-20 Length: 372
 Score: 317.00 Matches: 112
 Percent Similarity: 41.32% Conservative: 57
 Best Local Similarity: 27.38% Mismatches: 126
 Query Match: 12.58% Indels: 114
 Gaps: 15

US-09-935-124A-1 (1-1422) x US-09-973-063-4 (1-372)
 180 CTGCTCTTTGATGAC-----CTCCTCGGCGCAGCATCTAGCTCA----- 221
 Db 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
 222 -----GATCCAGGGGACCTTGTCTTTTGAATGAT----- 251
 Db 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrThrPheAspPheGlyIle 66
 252 -----CTCCACCGCTACGACGTGGCATTCAGT 281
 Db 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
 282 TCTCTGCCATCAATATGCCAGATGTAAAGACTGAAGGAAAGAGCAAGAAAA 341
 Db 81 -----LysTyrGly-----LysProIleProLysIle 90
 342 ACCTCCGAGAAAGAGAAATGAGCGATGAGAGCTTGTGAAAAAGAAAGTTGTAAGCC 401
 Db 82 -----LysTyrGly-----LysProIleProLysIle 90
 402 TCTTCGGTATCTTTGGCTGGAAGGGCTATGGCTGAGCGGAAGGGTGAAGGAGAG 461
 Db 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgLys-----GluAsnGluAsp 109
 462 ATGCAGATGCCACGTCATCTCTGAAGACATCCAGGAGAGTGAAGGCCCATGCTCC 521
 Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
 522 CTCATTACTCGGGTTTCATATTTTGTCTTTTATGATGACATGAGCAATCGAGCTCA 581
 Db 120 -----ValLeuTyrPheAlaValTyrAspGlyAsnGlyGlyProAlaAlaAla 135
 582 AAATTTGTCACAGAAATTTGCATCAAAATTATCAAGAAATTTCTTAAGAGATGTA 641
 Db 136 AspPheCysHisThrIleMetGluLysCysIleMetAspLeuPheProLys----- 152
 642 ATCAAGTGTAGAAAACCGTGAAGAGATGCTTTTGGACATTTCAAGCATACTATGA 701
 Db 153 -----GluLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGlnIleAspLys 169
 702 GAGTTCCTTAACAAGCT-----TCCAGCCAGAAAGCTCCTGGAAAGATGGGCTCACT 755
 Db 170 AlaPheSerSerHsAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
 756 GCCACGTGTGTGCTGTGCTGTAGACAACTT-----CTTATATTTGCCACCTCGAGATAGT 812

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Db 190 AlaThrValAlaLeuLeuArgSerGlyIleGluLeuValAlaLaserValGlyAspSer 209
QY CGGGCAATCTTGTGCTGTTATATAGAGAGATCAAAACATGCACCTTAAGCCCTCAGC 872
Db 210 ArgAlaIleLeuCyArg-----LysGlyLysProMetCysLeuThr 223
QY 873 AAAGACATTAATCCATCTAGATGAGAGCCGATGAGATACAGAGCCCTGAGAGA--- 929
Db 224 IleAspHisThrProGluArgLysSerGlyLysGluArgIleLysCysGlyIlePhe 243
QY 930 -----AAGCTCAGGAGTGGCGGTGTTGGCGGTGCTAAGAGTGTACAGCTCC 977
Db 244 ValAlaTrpAsnSerLeuGlnProHisValAsnGlyArgLeuLysMetThrArgSer 263
QY 978 ATTGGGAGCGGAGATGACAGCTGCGGTGCTACCTGTGTCGCGACATCAGAGCTGC 1037
Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTTGGCTGTGATGGCTCTTCAAGCTC 1094
Db 284 LysLeuHisIleValAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTTAACCCAGAAAGAGCCGTGAATCTTCTGCTGTCTCGAGATGAAAAGATCCAG 1154
Db 304 ValAsnSerGlnIleLysCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
QY 1155 ACCCGGAAAGGAAATGCCGACCGACCGCCGCTAGAGACCTGCAGAGCTGGCC 1214
Db 322 -----AlaAlaHisAlaValIleThr 327
QY 1215 AACAGCGGTGACGAGCGGCTCGCCGACAAAGCTAGTGTGTGTGTCGCGATAGGG 1274
Db 328 GluGlnAlaIleGluThrGlyThrGluAspSerThrAlaValValIleProPheGly 347
QY 1275 CACTGAGGGGTGGCGCGCCGACGAGG 1301
Db 348 AlaTrpGlyLysTrpLysAsnSerGlu 356

RESULT 15
US-09-973-964-4
; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-964-4

Alignment Scores:
Pred. No.: 5,38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.33% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
DB: 10 Gaps: 15
US-09-935-124a-1 (1-1422) x US-09-973-964-4 (1-372)

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QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGACAGTACTGACTCA----- 221
Db 27 LeuLeuGlnAspAspArgArgValThrProThrCysHisAspSerThrSerLysProArg 46
QY 222 -----GGATCAGGGGACCTTTGCTTTTGTGATGAT----- 251
Db 47 CysSerArgPheAspProAspLysSerGlySerProAlaThrTrpAspAsnGluIle 66
QY 252 -----CTCCACCCGCTAGACAGTGGCATTCAGGT 281
Db 67 TrpAspAsnArgIleAspGluProIleLeuLeuProIleProSerIle----- 81
QY 282 TCTCTTGGCCATCAATATCCAGATGTGAAGAAGCTGAAGGAAAGAGAAAGAAA 341
Db 81 ----- 81
QY 342 ACCTCCGAGAAAGAGAAAGAAATGGCAGTGAAGCTTTGTGAAGAAAGAAAGTTGTAAAGCC 401
Db 82 -----LysTrpGly-----LysProIleProLysIle 90
QY 402 TCTTGGGTGATCTTTGCTGTGAAGGCTATGAGCTGAGCGGAGGTGAGAGGAGAG 461
Db 91 SerLeuGluAsnValGlyCysAlaSerGlnIleGlyLysArgLys-----GluAsnGluAsp 109
QY 462 ATGCAGAGTGGCCACGTCATCTGAAACGACATCACCGAGAGTGAAGCCCATCGTCC 521
Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
QY 522 CTCATTAATCTGGGTTTCATATTTTCTGTTTGTATGACATGACAGAAATTCAGACCTCA 581
Db 120 -----ValLeuLysPheAlaValIleArgSerGlyHisGlyIleProAlaIleAla 135
QY 582 AAATTGTCGACACAAATTTGATCAAAATTAACAGAAATTTCCAAAGGAATGTA 641
Db 136 AspPheCysHisThrHisMetGluLysCysIleMetAspLeuLeuProLys----- 152
QY 642 ATCACTGTAGAGAAACCGTAGAGATGCTTTTGGACACTTTTCAGACATAGTAA 701
Db 153 -----GluLysAsnLeuGlnThrLeuLeuThrIleAlaPheLeuGlnIleAspLys 169
QY 702 GAGTTCCTTAAACAGCT-----TCCAGCCAGAAAGCTGCTGGAAGAAAGTGGTCACT 755
Db 170 AlaPheSerSerHisAlaArgLeuSerIleAspAlaThrLeuLeuThrSerGlyThrThr 189
QY 756 GCCAGGTGTGTTGCGCGTGAACAACAT---CTTATATTTGCCAAGCTGGAGATAGT 812
Db 190 AlaThrValAlaLeuLeuArgSerGlyIleGluLeuValAlaLaserValGlyAspSer 209
QY 813 CGGGCAATCTTGTGCTGTTATATAGAGAGATCAAAACATGCACCTTAAGCCCTCAGC 872
Db 210 ArgAlaIleLeuCyArg-----LysGlyLysProMetCysLeuThr 223
QY 873 AAAGACATTAATCCATCTAGATGAGAGCCGATGAGATACAGAGCCCTGAGAGA--- 929
Db 224 IleAspHisThrProGluArgLysSerGlyLysGluArgIleLysCysGlyIlePhe 243
QY 930 -----AAGCTCAGGAGTGGCGGTGTTGGCGGTGCTAAGAGTGTACAGCTCC 977
Db 244 ValAlaTrpAsnSerLeuGlnProHisValAsnGlyArgLeuLysMetThrArgSer 263
QY 978 ATTGGGAGCGGAGATGACAGCTGCGGTGCTACCTGTGTCGCGACATCAGAGCTGC 1037
Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTTGGCTGTGATGGCTCTTCAAGCTC 1094
Db 284 LysLeuHisIleValAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTTAACCCAGAAAGAGCCGTGAATCTTCTGCTGTCTCGAGATGAAAAGATCCAG 1154
Db 304 ValAsnSerGlnIleLysCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321

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QY 1155 ACCCGGAGGAGAGTCCGACGCCGCGCTACGAAGCCTTCGACAGGCTGGCC 1214
DB 322 -----AlaAlaHisAlaValThr 327
QY 1215 AACAAAGCGGTGACAGCGGGCTCGCGCCAGCAACGACTGTGATGGTGGCGGATAGG 1274
DB 328 GluGlnAlaIleGlnIrrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
QY 1275 CACTGAGGGGTGGCGCGCGGACGAG 1301
DB 348 AlaTrpGlyLysTrpLysAsnSerGlu 356

RESULT 16
US-09-975-072-4
; Sequence 4, Application US/09975072
; Patent No. US20020115607A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE OF INVENTION: Diseases
; CURRENT APPLICATION NUMBER: US 09/975,072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-072-4

Alignment Scores:
Pred. No.: 5,38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.32% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
DB: 10 Gaps: 15

US-09-935-124a-1 (1-1422) x US-09-975-072-4 (1-372)
QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGCGCCAGCAAGTACTGCTCA----- 221
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
QY 222 -----GATCAAGGGGAGCTTTGCTTTTGTATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnPheGlyIle 66
QY 252 -----CTCCACCGCGCTAGCAGTGGCGATTACAGT 281
DB 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTTCCACATCAATATCCAGATGTTAAAGCTGAAGGAGAAAGACAAAGAGAAA 341
DB 81 ----- 81
QY 342 ACCTCCGAGAGAGAGAGATGCGAGTGAAGACTTGTGAAAAGATTGTGAAGCC 401
DB 82 -----LysTrpGly-----LysProIleProLysIle 90
QY 402 TCTTCGGTATCTTTGGTCTGAAGGGCTATGCTGAGCGGAGAGGAGAGAGAGAG 461
DB 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgLys-----GluAsnGluAsp 109
QY 462 ATGACAGATCCACAGCTATCTGAAGCAATCAAGGAGAGAGTGAAGGCCCCCATCTCC 521
DB 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119

QY 522 CTCAATACCTGGGTTTCATATTTTGTCTTTTGTATGACATGAGAGATTCGACCTCA 581
DB 120 -----ValLeuTrpPheAlaValIrrAspGlyHisGlyValProAlaAlaIle 135
QY 582 AAATTTGCTGCACAGAAATTTGCATCAAAACTTAATCAAGAAAATTTCTTAAGAGATGA 641
DB 136 AspPheCysHisThrHisIleMetGlnLysCysAlaLeuAspLeuLeuProLys----- 152
QY 642 ATCAGTGTAGAGAAAACCGTGAAGAGATGCTTTTGTGACACTTTCAGCATATGATGAA 701
DB 153 -----GluLysAsnLeuGlnIrrThrLeuLeuThrIleuAlaPheLeuGlnIleAspLys 169
QY 702 GAGTTCCTTAACAGACT-----TCCAGCCAGAGGCTGCTGGAAGAGTGGCTCACT 755
DB 170 AlaPheSerSerHisAlaArgLeuSerIleAspAlaThrLeuLeuThrSerGlyThrThr 189
QY 756 GCCACGTGTGTCTGCTGTGATGACAACTT-----CTTATATTTGCCACCTCGAGATAGT 812
DB 190 AlaThrValAlaLeuLeuAspGlyIleGluLeuValValAlaSerValGlyAspSer 209
QY 813 CGGCAATCTTGTGCTGTATATGAGAGAGTCAAAAACATGACAGCCCTTAAGCTCAGC 872
DB 210 ArgAlaIleLeuGlyArg-----LysGlyLysProMetLysLeuThr 223
QY 873 AAAGAGCATATCAACTCAGTATGAGAGCGGATGAGTACAGAAAGCTTGAGGA--- 929
DB 224 IleAspHisThrProGluLysArgAspGluLysGluLysGlyGlyPhe 243
QY 930 -----AACGTACAGGATGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
DB 244 ValAlaTrpAsnSerLeuGlyGlnProHisAlaValAsnGlyArgLeuAlaMetThrArgSer 263
QY 978 ATTGGGACCGGCGATGACAAAGCGCTGCGTGTCACTCTGTGCGCCGACATCAAGCTGC 1037
DB 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTTTCATTTTGTGCGCTGTGATGGGCTTCAAGGTC 1094
DB 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTTAACCCAGAGAGACCGCTGAACCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1154
DB 304 ValAsnSerGlnGlnIleCysAspPheValAsnGlnIrrHisAspProAsnGlu----- 321
QY 1155 ACCCGGAGGAGAGTCCGACGCCGCGCGCTACGAAGCCTTCGACAGGCTGGCC 1214
DB 322 -----AlaAlaHisAlaValThr 327
QY 1215 AACAAAGCGGTGACAGCGGGCTCGCGCCAGCAACGACTGTGATGGTGGCGGATAGG 1274
DB 328 GluGlnAlaIleGlnIrrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
QY 1275 CACTGAGGGGTGGCGCGCGGACGAG 1301
DB 348 AlaTrpGlyLysTrpLysAsnSerGlu 356

RESULT 17
US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE OF INVENTION: Diseases
; CURRENT APPLICATION NUMBER: US 09/972,038
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-038-4

Alignment Scores:
  Pred. No.:      5,38e-20      Length:      372
  Score:          317.00        Matches:     112
  Percent Similarity: 41.32%    Conservative: 57
  Best Local Similarity: 27.38%  Mismatches:  126
  Query Match:    12.38%       Indels:      114
  DB:              10          Gaps:          15

US-09-935-124A-1 (1-1422) x US-09-972-038-4 (1-372)

QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGCAGTCACTCA----- 221
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
QY 222 -----GGATCAGGGGGACCTTTGCTTTTGATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnPhcGlyLe 66
QY 252 -----CTCCACCCGCTAGCAGTGGCCATTGAGT 281
DB 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTTGCCACATCATATATCCAGATGTAAAGACTGAAGGAAAGAGCAAAAGAAAA 341
DB 81 ----- 81
QY 342 ACCTTCGAGAAAGAGAAGATGGCAGTGAAGACTTGTGAAAAGAAAGTTGTTAAAGCC 401
DB 82 -----LysTyrGly-----LysProIleProGlyLe 90
QY 402 TCTTCGGTATCTTTGGTGTGAAGGGCTATGTGGCTGAGCGGAAGGGGTGAAGGGAGAG 461
DB 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgLys---GluAsnGluAsp 109
QY 462 ATGCAGAGATGCCAGCTATCCGAAAGCATGACGAGAGAGTGAAGGCCCATGCTCC 521
DB 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
QY 522 CTCATTACTCGGGTTTCATATTTTGTGTTTGATGATGACATGAGAAATTCGAGCCTCA 581
DB 120 -----ValLeuYrPheAlaValTyrAspGlyHisGlyLysProAlaAlaAla 135
QY 582 AAATTTGTCGACAGATTTGCTCAAAATTATATCAAAAATTTCTTAAAGAGATGTA 641
DB 136 AspPheCysHisThrHisMetGlnLysCysIleMetAspLeuLeuProLys----- 152
QY 642 ATCAGTGTAGAGAAACCGTGAAGAGATGCTTTTGGACACTTTCAGACTATCTGTA 701
DB 153 -----GluYrAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGluIleAspLys 169
QY 702 GAGTTCCTTAAACAGCT-----TCCAGCCAGAAAGCTGCTGAGAAAGAGTGCCTCACT 755
DB 170 AlaPheSerSerHisIleAspArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
QY 756 GCCACGTGTGTTGCTGCTGATAGCAACATT--CTTTATATTGCCAAGCTCGAGATAGT 812
DB 190 AlaThrIleValIleLeuLeuArgAspGlyIleGluLeuValIleAlaSerValGlyAspSer 209
QY 813 CGGGCAATTTGTGTGCTATATAAGAGAGTCAAAACATGACAGCTTAAAGCCTTAC 872
DB 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetLeuLysLeuThr 223
QY 873 AAAGAGCATATTCACACTAGTATGAGAGCGGATGAGATCAGAAAGCTGAGAGAGAGAG 929
DB 224 IleAspHisThrProGluArgLysAspGlyLysGluArgIleLysLysCysGlyGlyPhe 243
QY 930 -----AACGTCAAGGATGGCGTGTGTTGGCGGTGTAGAGGTGTCAAGCTCC 977

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DB 244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
QY 978 ATTTGGGAGCGGACAGTGAAGAGGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1037
DB 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGlnThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGTTCATTTGTTGGCTGTGATGGCTCTTCAAGGTC 1094
DB 284 LysLeuHisIleAlaAspAspSerPheLeuValLeuThrTrpAspGlyIleAsnPhcMet 303
QY 1095 TTTACCCCAAGAAAGACCGTGAACCTTCATCTTGTCTGTCTGAGAGTGAAGATCCAG 1154
DB 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
QY 1155 ACCCGGAAAGGAGAGTCCGACCCGACCGCCGCTAGAAAGCAGTGCAGAGCTGGCC 1214
DB 322 -----AlaAlaHisIleValThr 327
QY 1215 AACAGCGCGTGCAGCGGGGCTCGGCCGACAACTGATGTGATGTGGTGGATAGGG 1274
DB 328 GluGlnAlaIleGlnTyrGlyThrGluAspAsnSerThrAlaValValProPhcGly 347
QY 1275 CACTGAGGGGTGGCGCGCGCCAGAG 1301
DB 348 AlaTrpGlyLysTyrLysAsnSerGlu 356

RESULT 18
US-09-972-757-4
; Sequence 4, Application US/09972757
; Patent No. US2002011927A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,757
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-757-4

Alignment Scores:
  Pred. No.:      5,38e-20      Length:      372
  Score:          317.00        Matches:     112
  Percent Similarity: 41.32%    Conservative: 57
  Best Local Similarity: 27.38%  Mismatches:  126
  Query Match:    12.38%       Indels:      114
  DB:              10          Gaps:          15

US-09-935-124A-1 (1-1422) x US-09-972-757-4 (1-372)

QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGCAGTCACTCA----- 221
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
QY 222 -----GGATCAGGGGGACCTTTGCTTTTGATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnPhcGlyLe 66
QY 252 -----CTCCACCCGCTAGCAGTGGCCATTGAGT 281
DB 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTTGCCACATCATATATCCAGATGTAAAGACTGAAGGAAAGAGCAAAAGAAAA 341

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Db 81 ----- 81
Qy 342 ACCTCGAGAGAGAAATGCGAGTGAAGCTTGTGAAAAGAAAGTTGTAAAGCC 401
82 -----LysTyrGly-----LysProIleProIle 90
Qy 402 TCTTCGGTGAATCTTGGCTGAAGGGCTATGTGGCTGAGCGGAGGGGTGAGAGAGAG 461
91 SerLeuGluAenValGlyCysAlaSerGlnIleGlyLysArgLys---GluAenGluAer 109
Qy 462 ATCCAGAGATGCCAGATGATCCGGAACGATACCGAGAGAGATGAGGCCCATGTC 521
110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
Qy 522 CTCATTACTCGGGTTTCATATTGGCTGTGTGATGAGCATGAGAGAAATTCGAGCTCA 581
120 -----ValLeuTyrPheAlaValTyrAspGlnIleGlyProAlaAla 135
Qy 582 AAATTGCTGCACAGAAATTCGATCAAAACTTAATAGAAAATTTCTTAAAGAGATGA 641
136 AspPheCysHisThrHisMetGluLysCysAlaLeuAspLeuLeuProLys----- 152
Qy 642 ATCAGTGTAGAGAAAACCGTAGAGATGCCCTTTGACACTTTCAGACTCTGATGA 701
153 -----GluLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGluLysAsp 169
Qy 702 GAGTTCCTTAAACAGCT-----TCCAGCCAGAACCGCTGCGAAAGATGGCTCACT 755
170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyTyrThr 189
Qy 756 GCCACGTGTGTGCTGCTGTGATGACAACTT-----CTTTATATTTCCCACTCGAGATAGT 812
190 AlaThrValAlaLeuLeuAspArgProIleGluLeuValValAlaSerValGlyAspSer 209
Qy 813 CGGCGCATCTTGTGTGTTATATGAGAGAGTCAAAAACATGACACCTTAAAGCTCAGC 872
210 ArgAlaIleLeuLysArg-----LysGlyLysProMetLeuLeuThr 223
Qy 873 AAAGAGCATATCCAGTCAATGATGAGAGCGGATGAGATGAGATGAGATGAGATGAG 929
224 IleAspHisThrProGluArgLysAspGlnLysGlnIleLysLysCysGlyGlyPhe 243
Qy 930 -----AACGTGAGAGATGGCGTCTTTGGCGGTGCTGAGATGAGATGAGCTGC 977
244 ValAlaThrAsnSerLeuGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
Qy 978 ATTGGGAGCGGAGATGACAGCGCTGCGGTCTCACTGTGCGCCGACATGACAGCTGC 1037
264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGlnProGluThrLysArgGly 283
Qy 1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTGAGCTGTGATGGCTCTTCAAGCTC 1094
284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrArgSerPheMet 303
Qy 1095 TTATCCCGAGAGAGCCGTGAATCTTCACTTGTCTGTCTCGAGATGAAAAGATCCAG 1154
304 ValAsnSerGlnGlnIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
Qy 1155 ACCCGGAGAGGAGATGCCGAGCCGACCGCGCTACGACAGCTGCAAGCTGCGCC 1214
322 -----AlaAlaHisAlaValThr 327
Qy 1215 AACMAGCGGTGAGCGGGGTGCGCCGACAACTGATGATGATGATGATGATGATGATG 1274
328 GluGlnAlaIleGlnIlyrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
Qy 1275 CACTGAGGGGTGCGCGCGCGCGCGAG 1301
348 AlaTyrPheLysTyrTyrAsnSerGlu 356
RESULT 19
US-09-973-965-4

Sequence 4, Application US/09973965
Patent No. US20020124273A1
GENERAL INFORMATION:
APPLICANT: Roche, Jean-Marc
APPLICANT: Bartel, Paul L.
APPLICANT: Heichman, Karen
TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
FILE REFERENCE: Protein Interactions in ND
CURRENT APPLICATION NUMBER: US/09/973,965
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/240,790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: US 60/304,775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
US-09-973-965-4
Alignment Scores:
Pred. No.: 5,39e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.32% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
Gaps: 15
US-09-935-124a-1 (1-1422) x US-09-973-965-4 (1-372)
Qy 180 CTGCTCTTGAATGAC-----CTCCCTCGGCGACGAGTACATCACTCA----- 221
Db 27 LeuLeuGlnAspArgArgValThrProThrCysHisSerSerHisSerGlnProArg 46
Qy 222 -----GATCAGCGGAGCTTTCTCTTTGAATGAT----- 251
Db 47 CysSerArgPheAspProAspArgLysSerProAlaThrThrAspAsnPheGlyIle 66
Qy 252 -----CTCCACCCGCTGACGATGCGGATTCAGT 261
Db 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
Qy 282 TCTCTGCCATCATCATATCCAGATGGTAAAGACTGAAGGAGAAAGAGAGAAAA 341
Db 81 ----- 81
Qy 342 ACCTCGAGAGAGAAATGCGAGTGAAGCTTGTGAAAAGAAAGTTGTAAAGCC 401
Db 82 -----LysTyrGly-----LysProIleProIle 90
Qy 402 TCTTCGGTGAATCTTGGCTGAAGGGCTATGTGGCTGAGCGGAGGGGTGAGAGAGAG 461
91 SerLeuGluAenValGlyCysAlaSerGlnIleGlyLysArgLys---GluAenGluAer 109
Qy 462 ATCCAGAGATGCCAGATGATCCGGAACGATACCGAGAGAGATGAGGCCCATGTC 521
110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
Qy 522 CTCATTACTCGGGTTTCATATTGGCTGTGTGATGAGCATGAGAGAAATTCGAGCTCA 581
120 -----ValLeuTyrPheAlaValTyrAspGlnIleGlyProAlaAla 135
Qy 582 AAATTGCTGCACAGAAATTCGATCAAAACTTAATAGAAAATTTCTTAAAGAGATGA 641
136 AspPheCysHisThrHisMetGluLysCysAlaLeuAspLeuLeuProLys----- 152
Qy 642 ATCAGTGTAGAGAAAACCGTAGAGATGCCCTTTGACACTTTCAGACTCTGATGA 701
153 -----GluLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGluLysAsp 169

QY 702 GAATTCCTTAACAGCT-----TCAGCCAGAACCTGCTGGAAGATGGCTCACT 755
Db 170 AAlPhSeSerxiValAArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
QY 756 GCCACGTGTGTTGGCTGTAGACAATT---CTTTATATGGCAACCGGAGATAG 812
Db 190 AlAthValAlaLeuLeuArgAspGlyIleGlyLeuValValAlaSerValGlyAspSer 209
QY 813 CGGGCAATCTTGTGCTTATTAATGAGAGACTCAAAAATGACAGCTTAAGCCTCAGC 872
Db 210 ArgAlaIleLeuGlyValArg-----LysGlyLysProMetLysLeuThr 223
QY 873 AAAGACATATATCAACTGATGAGAGCCGATGAGATACAGAGCGTGGAGCA--- 929
Db 224 ILeAspHleThrProGlyArgGlyValGlyAlaGlyIleLysLysCysGlyGlyPhe 243
QY 930 -----AACGTCAGGAGATGGCGCTTTGGCGGTGCTAGAGGTCAGCGCTCC 977
Db 244 ValAlaITrPheSerLeuGlyGlnProHleValAsnGlyArgLeuAlaMetThrArgSer 263
QY 978 ATTGGGAGCGGCGATGACAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1037
Db 264 ILeGlyAspLeuAspLeuSerGlyValIleAlaGlnProGlyThrArgGlyIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTCATTTTGGCTGATGAGCGCTTTCAAGTTC 1094
Db 284 LysLeuHleHleValAspAspSerPheLeuValLeuThrArgAspGlyIleAsnPheMet 303
QY 1095 TTATACCCAGAAAGACCGGTAATCATCTTGTCTGTCTGAGATGAAAAGATCCAG 1154
Db 304 ValAsnSerGlnGlnIleCysAspPheValAsnGlnCysHleAspProAsnGlu----- 321
QY 1155 ACCCGGAAAGGAGATGCCGAGCCGAGCCGCTAGAGACAGCTGCAACAGCTGGCC 1214
Db 322 -----AlaAlaHleValAlaValThr 327
QY 1215 AACAGCGCGTGCAGCGGGCTGCGCCGACAGCTGATGATGGTGGCGGATAGG 1274
Db 328 GlnGlnAlaIleGlnIleArgIleThrGlnAspAsnSerThrAlaValAlaIleProPheGly 347
QY 1275 CACTGAGGGGTGGCGGCGCCAGGAG 1301
Db 348 AlaTrpGlyLysTrpLysAsnSerGln 356
RESULT 20
US-10-072-130-1
Sequence 1, Application US/10072130
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Golil, Surya K.
Lal, Preeti
Corley, Neil C.
Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/072,130
FILING DATE: 05-Feb-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093

FILED DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TAPIPLB01
CLONE: 131177
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-072-130-1
Alignment Scores:
Pred. No.: 1,35e-19 Length: 478
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: 8 Gaps: 8
US-09-935-124A-1 (1-1422) x US-10-072-130-1 (1-478)
QY 333 AAGAGAAACCTCCGAGAGAGAGAAATGGCACTGAGAGCTTGTGAAAGAAAGTT 392
Db 7 LysProlLysThrGlnLysHleAsnAlaHleGlyAlaGlyAsn----- 20
QY 393 TGTAAAGCTCTGGGTATCTTTGTCTGAAAGGCTATGTGGCTGAGCGGAAGGTGAG 452
Db 21 -----GlyLeuArgGlyGlyLeuSerSerMetGlnIleThr 32
QY 453 AAGGAGAGATGACAGATGCCACGCTCATCTGAAAGCATCACCGAGAGTGAAGCCC 512
Db 33 ArgValAlaGlnMetGlnAspAlaHleThrAlaValAlaGlyIle----- 46
QY 513 CGATGTCCTCATTAATCTGGGTTTCATATTTTGTCTGTTTGTATGACATGAGGAATT 572
Db 47 ProHleGlyLeu---GlnAspTrpSerPhePheAlaValIleArgGlyHleAlaGlySer 65
QY 573 CGAGGCTCAAAATTTGCTGCGACAGAAATTGCATCAAACTTAATCAG----- 620
Db 66 ArgValAlaAsnTrpCysSerThrHleLeuLeuGlnHleIleThrAsnGlnAspPhe 85
QY 621 -----AAATTCCTTAAGAGATGTAATCAGTGTAGAGAAACCGTGAAGAGA 668
Db 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGlnLeuSerValGln---AsnValLysAsn 104
QY 669 TGCCTTTGGACATTTCAAGCATCTGATGAAGATTCCTTAACAGCTTCCAGCCAG 728
Db 105 GlyIleArgThrGlyPheLeuLysIleAspGlyIleArgAsnAspSerAspLeuArg 124
QY 723 AAGCTGCTGGAAGAAGATGGTCCCTGCCAGCTGTGTTGGCTGTAGACAACATTCT 788
Db 125 AsnGlyMetAspArgSerGlySerThrAlaValGlyValMetIleSerProLysHleIle 144
QY 789 TATATTGCCAAGCTCGAGATAGTGGGCAATCTTGTGCTTATTAATGAGAGAGTCA 848
Db 145 TyrPheIleAsnCysGlyAspSerArgAlaValLeuTyrArgAsnGlyGln----- 161
QY 849 AAACATGACAGCTTAAGCTCAGCAAGAGCATTAATCCAACATCAGATGAAGCGGATG 908
Db 162 -----ValCysPheSerThrGlnAspHleLysProCysAsnProArgGlnLysGln 178
QY 909 AGGATACAGAGGCTGAGAGAAAGTCAGAGATGGCGCTGTTTGGCGGTGCTAAGGTG 968
Db 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198


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Db      267 AepLeuGlubAnValCybaentPrValIaBpThCyLeuHiSlyeGlySerArgAsp 286
Qy      1245 AACGTCACTGTAGTGCTG 1265
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Db      287 AsnMetSerLeuValLeuVal 293

RESULT 22
US-09-925-300-1655
; Sequence 1655, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1655
; LENGTH: 373
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (290)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (325)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1655

Alignment Scores:
Pred. No.: 1,49e-19 Length: 373
Score: 312.00 Matches: 112
Percent Similarity: 40.83 Conservative: 55
Best Local Similarity: 27.38 Mismatches: 128
Query Match: 12.198 Indels: 114
De: 10 Gaps: 15

US-09-935-124a-1 (1-1422) x US-09-925-300-1655 (1-373)
Qy      180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGCACTGTAAGTCA----- 221
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Db      28 LeuLeuGlnAspArgValIlnProThCyHisSerSerThrSerGluProArg 47
Qy      222 -----GGATCAGGGGACCTTTGCTTTGATGAT----- 251
      |||:|||||:|||||
Db      48 CySerArgPheAspProAspGlySerGlySerProIaIlnTrpAspAsnPheGlyIle 67
Qy      252 -----CTCCACCCCGCTAGCAGTGCAGTTCAGGT 281
      |||:|||||:|||||
Db      68 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 82
Qy      282 TCTCTTCCCATCATATATCCAGATGTTAAAGACTGAAGGAAAGAGCAAGAAAA 341
      |||:|||||:|||||
Db      82 ----- 82
Qy      342 ACCTCGAGAGAGAGAAGATGCGACGTGAAGAGCTTGTGAAAGAAAGTTGTAAAGCC 401
      |||:|||||:|||||
Db      83 -----LysTyrGly-----LysProIleProIleProIle 91
Qy      402 TCTTCGGTATCTTTGGTCTGAAGGCGCTATGTGCTGACGGAAAGGCTGAGAGGAGAG 461

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Db      92 SerLeuGluAsnValGlyCySerIaSerGlnIleGlyLysArgLys---GluAsnGluAsp 110
      |||:|||||:|||||
Qy      462 ATGCAGAGATGCCAGGTGATCTCTGAACGACATCACCGAGGATGTAAGGCCCATGTGCC 521
      |||:|||||:|||||
Db      111 ArgPheAsp-----PheAlaGlnLeuIlnTrpAspGlu----- 120
Qy      522 CTCATTAATCTCGGGTTTCATATTGCTGTGTTTGAATGACATGAGAGAAATTCAGACCTCA 581
      |||:|||||:|||||
Db      121 -----ValLeuTyrPheAlaValTyrAspGlyHisGlyGlyProAlaIlaIla 136
Qy      582 AAATTGCTGCACAGAAATTTGCAATAAACTTAATCAGAAAAATTTCTTAAGAGAAATGTA 641
      |||:|||||:|||||
Db      137 AspPheCyHisIleThiHleMet**LysCySIIeMetAspLeuLeuProLys----- 153
Qy      642 ATCAGGTGTAAGAAACCGTGAAGAGATGCGCTTTTGACACTTGAAGATGCTGATGAA 701
      |||:|||||:|||||
Db      154 -----GlnLysAsnLeuGlnIlnTrIleuLeuIlnTrIleuAlaPheLeuGlnIleAspLys 170
Qy      702 GAGTTCCTTAAACAAGCT-----TCCAGCCGAAGCCCTGGAAGATGCGTCACT 755
      |||:|||||:|||||
Db      171 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaIlnTrIleuLeuThrSerGlyIlnTrIln 190
Qy      756 GCGACGGTGTGTTGCGCTGTAGCAACAT--CTTATATTGCCAAGCTCGAGATAGT 812
      |||:|||||:|||||
Db      191 AlaIlnTrValAlaLeuLeuArgAspGlyIleGlnLeuValAlaIleSerValGlyAspSer 210
Qy      813 CGGGCAATCTGTGTCGTTATTAATGAGAGAGTCAAAACATGACGACCTTAAGCCCTGACG 872
      |||:|||||:|||||
Db      211 ArgAlaIleLeuCyArg-----LysGlyLysProMetLysLeuIlnTr 224
Qy      872 AAAGACATATCTCACTAGTATGAGAGCGAGATGAGATGAGATGACAGAAAGCTGAGAGA-- 929
      |||:|||||:|||||
Db      225 IleaRphIleThrProGlnArgLysAspGlnLysGlnArgIleLysLysCysGlyGlyPhe 244
Qy      930 -----AACGTACAGGATGCGCGTGTGCGCGCTCTTAAGGTGTACAGCTCC 977
      |||:|||||:|||||
Db      245 ValAlaIlnTrAsnSerLeuGlyGlnProIlnValaGlnArgLeuAlaIleMetThrArgSer 264
Qy      978 ATTTGGGAGCGGCGACATPACAGCGCTGCGGTGCACCTGTGCGCGACATGACAGCTGTC 1037
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Db      265 IlegIlyAspLeuAspLeuIlnTrSerGlyValIleAlaGluProGluIlnTrLysArgIle 284
Qy      1038 CAGCTG---ACCCCAATGACAGTTCATTTGTTGCGCTGATGAGGCTCTTCAAGTTC 1094
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Db      285 LysLeuHisHisAla**AspSerPheLeuValLeuIlnTrIlnAspGlyIleAsnIlnMet 304
Qy      1095 TTTACCCCAAGAAAGACCGGTGACTTTCATTTGCTGCTGCTGCGAGATGAAGATCCAG 1154
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Db      305 ValaAsnSerGlnGluIleCyAspPheValaGlnIlnTrIlnAspProAsnGlu----- 322
Qy      1155 ACCCGGAAAGGGAAGTCCGACCGACCGCCGCTGAAGAGCGCTGCAAGCGGTGGCC 1214
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Db      323 -----AlaAla**AlaVal*** 328
Qy      1215 AACAAAGCGGTGACAGCGGCTCGGCCGACATGCACTGTGATGATGCGGTGCGGATAGG 1274
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Db      329 GlnGlnAlaIleGlnIlnTrGlyIlnTrGlnAspAsnSerIlnAlaValaValaProIlnGly 348
Qy      1275 CACTAGAGGGGTGCGCGCGGCGGACGAG 1301
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Db      349 AlaIlnTrGlyLysTyrLysAsnSerGlu 357

RESULT 23
US-09-925-300-1254
; Sequence 1254, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300

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Db 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetLysLeuThr 223
QY 873 AAAGAGCTTATTCGACTGCTATGAAAGCCGAGTACAGAGCGCTGGAGGA--- 929
Db 224 IleAspHisThrProGluArgLysAspGluLysGluArgLysCysGlyGlyPhe 243
QY 930 -----AACGTGAGGAGTGGGCGGTGTTGGGCGGTGCTAAGGTGTCAAGCTGC 977
Db 244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
QY 978 ATTGGGACGGGCGAGTACAAAGCGCTGGGTGCTGACCTGTGCTCCGACATCAGACGCTGC 1037
Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTTGGCGCTGAGATGGGCTCTTCAAGTTC 1094
Db 284 LysLeuHisLeuIleAlaAspAspSerPheLeuValIleuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTACCCCGAAGAGACCGGTGACTTCATCTGTGCTGCTG 1133
Db 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCys 316
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Search completed: February 9, 2003, 18:12:41
Job time : 37.5 secs

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/ NUMBER OF SEQ ID NOS: 2318
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1562
/ LENGTH: 441
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US01-01239-1562

Alignment Scores:
Pred. No.: 5,32e-171 Length: 441
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
DB: 1 Gaps: 0

US-09-935-124A-1 (1-1422) x PCT-US01-01239-1562 (1-441)

QY 9 GCCCGCTGCTGCCGCCGCCGCCGGGTGTGAGCCCGCGCTGCTGCGGGCTGAGTGTG 68
DB 19 AIAARGCYsAARGProProGlyValITrPserProAlaAlaAlaArgGlyLeuSerVal 38
QY 69 TGTGCTGTGCGCGCGCTCCACCCAGCCTCCGCGATGAGCCTTTCGGGGACCTGCGCGAG 128
DB 39 CybAArgCybAArgLeuHISProAlaSerAlaMetAspLeuPheGlyAspLeuProGlu 58
QY 129 CCGAGCGCTCGCGCGCGCGCGCTGCGCGGAAAGAGCTCAGAAAGAGACCCCTGCTCTT 188
DB 59 ProGluAArgSerProAlaArgProAlaAlaGlyLyGluAlaGlnLySerGlyProLeuLeuPhe 78
QY 189 GATGACCTCTCTCCGCGCAGCAGTACTGACTCAGATCAGGGGACCTTTCCTTTTGTAT 248
DB 79 AspAspLeuProProAlaSerSerThrAspSerGlySerGlyProLeuLeuPheAsp 98
QY 249 GATCTCCGACCCGCTGAGCAGTGGCGATTCAGTCTCTTTCGACATCAATATCCAGATG 308
DB 99 AspLeuProProAlaSerSerGlyAspSerGlySerLeuAlaThrSerIleSerGlnMet 118
QY 309 GTAAGAGCTGAAGGAGAAAGAGCAAGAAAGAACTCCGAGAGAGAGAGATGACAGT 368
DB 119 ValLyThrGlnGlnLySerGlyAlaLySerGlyThrSerGlnGlnGlnLySerGln 138
QY 369 GAAAGAGCTTGTGAAAGAAAGTTTGTAAAGCTTTCGCTGATCTTTCGCTGAGAGGC 428
DB 139 GlnGlnLeuValGlnLySerValCybLyAlaSerSerValIlePheGlyLeuLySerGly 158
QY 429 TATGTGCGTGAAGCGGAGGAGTGAAGAGAGAGATGACAGAGTCCACATCCCTGAAG 488
DB 159 TyrValAlaGlnLySerGlyValArgGlnGlnMetGlnAspAlaHisValIleLeuAsn 178
QY 489 GACATCACCAGAGAGTGTAGGCCCCCATCGTCCCTCATTAATCGGGTTTCATATTGGCT 548
DB 179 AspIleThrGlnGlnLySerArgProProSerSerLeuIleThrArgValSerTyrPheAla 198
QY 549 GTTTTGTGATGAGCATGAGAGAAATTCAGAGCTCAAAATTTGCTGACACAGAAATTTGACAA 608
DB 199 ValPheAspGlyHisGlyGlyIleArgAlaSerLyPheAlaIleGlnAsnLeuHisGln 218
QY 609 AACTTAATCAGAAATTTCTTAAGAGAGATGTAAATCAGTGTAGAGAAACCGTGAAGAGA 668
DB 219 AsnLeuIleArgLyPheProLySerGlyAspValIleSerValGlnLySerThrValLyAsp 238
QY 669 TGCCTTTGGACACTTTCAAGCATACTGATGAAGAGTTCTTAAACAGCTTCCAGCCAG 728
DB 239 CybLeuLeuAspThrPheLeuHisThrAspGlnGlnPheLeuLySerGlnAlaSerSerGln 258
QY 729 AAGCTGCTGGAAGAGATGGGTCACTGCCACGTGTGTTCTGGCTGTAGACAACTTCTT 788
DB 259 LybProAlaITrLyAspGlySerThrAlaThrCybValLeuAlaValAspLeuIleLeu 278
QY 789 TATATTGCCCACTCGGAGATAGTCCGGCAATTTGTGTGCTTATAATGAGAGAGATCAA 848
DB 279 TyrIleAlaAsnLeuGlyAspSerArgAlaIleLeuCybArgGlyTrAsnGlnGlnSerGln 298
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QY 849 AAATATGACGCTTAAGCCTCAGCAAGAGCATTAATCCAACTCAGTATGAAAGCGGATG 908
DB 299 LybHisAlaIleLeuSerLeuSerLybHisThrProThrGlnLySerGlnGlnArgMet 318
QY 909 AGGATATCAGAAAGCTGAGAGAAAGCTCAGAGATGGCGCTTTTGGCGCTGCTAAGGTG 968
DB 319 ArgIleGlnLybAlaGlyGlyAsnValArgAspGlyArgValLeuGlyValLeuGlyVal 338
QY 969 TCAGCTCCATTTGGGAGAGCGGAGAGTACAGCGCTGCGGGTCACTGTGTCGCCAGATC 1028
DB 339 SerArgSerIleGlyAspGlyGlnLybHisThrArgGlyValThrSerValProAspIle 358
QY 1029 AGAGCGCTGCAAGCTGACCCCAATGACAGTTTCATTTGTTGGCTGTGATGGGCTCTTC 1088
DB 359 ArgArgCybGlnLeuThrProAsnAspArgPheIleLeuLeuAlaCybAspGlyLeuPhe 378
QY 1089 AAGTCTTTTACCCGAGAAAGAGCCGTGAATTCATCTTGTCTGTCTGTGAGATGAANA 1148
DB 379 LybValPheThrProGlnGlnAlaValAsnPheIleLeuSerCybLeuGlnAspGlnLy 398
QY 1149 ATCCAGACCCCGGAGAGGAGAGTCCGACGCCAGCGCGCTACGAGACGCTGCAACAGG 1208
DB 399 IleGlnThrArgGlnGlyLybSerAlaAlaAspAlaArgTyrGlnAlaAlaCybAsnArg 418
QY 1209 CTGGCCAAACAAAGCGGCTGACAGCGGGCTCGCGCGACAACTGACTGTGATGGTGGCG 1268
DB 419 LeuAlaAsnLybAlaValGlnArgGlySerAlaAspAsnValThrValMetValValArg 438
QY 1269 ATAGGGCAC 1277
DB 439 IleGlyHis 441

RESULT 2
US-09-764-902-1562
/ Sequence 1562, Application US/09764902
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT213
/ CURRENT APPLICATION NUMBER: US/09/764,902
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2318
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1562
/ LENGTH: 441
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-764-902-1562

Alignment Scores:
Pred. No.: 5,32e-171 Length: 441
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
DB: 21 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-764-902-1562 (1-441)

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DB 19 AIAARGCYsAARGProProGlyValITrPserProAlaAlaAlaArgGlyLeuSerVal 38
QY 69 TGTGCTGTGCGCGCTCCACCCAGCCTCCGCGATGAGCCTTTCGGGGACCTGCGCGAG 128
DB 39 CybAArgCybAArgLeuHISProAlaSerAlaMetAspLeuPheGlyAspLeuProGlu 58
QY 129 CCGAGCGCTCGCGCGCGCGCGCTGCGCGGAAAGAGAGCTCAGAAAGAGACCCCTGCTCTT 188
DB 59 ProGluAArgSerProAlaArgProAlaAlaGlyLyGluAlaGlnLySerGlyProLeuLeuPhe 78
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QY	189	GANCTCCCTCCCGGCGACACACTATCTAGCTCAGAACTCAGGGAGACCTTTCCTTTTGAT	248
Db	79	AspAspLeuProProAlaIleSerSerThrAspSerGlySerGlyProLeuLeuPheAsp	98
QY	249	GATCTCCGACCCCGCTACGACTGGGCGATTGAGTTCTCTTCCGACATCAATATCCCAATG	308
Db	99	AspLeuProProAlaIleSerSerGlyAspSerGlySerLeuAlaThrSerIleSerGlnMet	118
QY	309	GTTAAACACTGAAGGGAAGAAGGCAAGAAAACCTCCGAGGAAGAAGAAATGGGAGT	368
Db	119	ValLeuThrGlnGlyLeuYsgGlyAlaValAspGlySerThrSerGlnGlnGlyAspGlnYser	138
QY	369	GAAAGCTTGTGGAAAAGAAAGTTTGTAAGCCTCTTCGGTGAATCTTTGGTCTGAAGGGC	428
Db	139	GlnGlnLeuValGlnValValValCysValAlaSerSerValIlePheGlyLeuValGly	158
QY	429	TATGTGGCTGACCGGAGAGGTGAGAGGGAGAGATGCAAGATGCCATCGTCACTCTGAC	488
Db	159	TyrValAlaGlnAlaYsgYsgYsgYsgGlnGlnGlnMetGlnAspAlaAlaValIleLeuAsn	178
QY	489	GACATCACCGAGAGACTGTAGAGGCCCCCATCGTCCCTCATTACTCGGGTTCAATATTTGCT	548
Db	179	AspIleThrGlnGlnCysArgProProSerSerLeuIleThrArgValSerYsrPheAla	198
QY	549	GTTTTCGATGAGCACAAGAGAAATTCGAGCCTCAAAATTTTGCCTGCACAGAAATTTGCATCA	608
Db	199	ValPheAspGlyHisGlyGlyIleArgAlaSerYsrPheAlaAlaGlnAsnLeuHisGln	218
QY	609	AACATTAATCAGAAAATTTCTTAAAGAGATGTAACTACGTAGAGAAAACCGCTGAAGAGA	668
Db	219	AsnLeuIleArgYsrPheProYsgYsrValIleSerValGlnYsrThrValYlsArg	238
QY	669	TGCTTTTGGACACTTTCACAGATACATGATGAAGAAGTTCTTAAACAGCTTCCAGCAG	728
Db	239	CysLeuLeuAspThrPheYsrHisIleThrAspGlnGlnPheLeuYsgIlnAlaSerSerGln	258
QY	729	AAGCTCCCTCGAAAGAATGGCTGACACCTGCCAGCGTGGTTCCTGGCTGAGACAACTTCTT	788
Db	259	LeuProAlaTrpYsrAspGlySerThrAlaIleThrCysValLeuAlaValaAspAsnIleLeu	278
QY	789	TATATTCGCAACTCGAGATATGTCGGGCAATCTTGTCGCTGTATATATGAGAGAGTCA	848
Db	279	TyrIleAlaAsnLeuYsrAspSerArgAlaIleLeuCysArgYsrAsnGlnGlnSerGln	298
QY	849	AAACATGACGCTTAAGCTCAGCAAAAGACATATCAACTCAGTATGAAGCGGGATG	908
Db	299	LeuSerAlaAlaLeuSerLeuSerYsgIlnHisAspProThrGlnYsrGlnGlnAspMet	318
QY	909	AGGATACGAAAGGCTGAGAGAAACCTCAGGAGTGGCGTGTTTGGCGTGTCAAGGGTG	968
Db	319	ArgIleGlnYsnYsaIagYsgYsaValaArgAspGlyArgValaLeuGlyValaLeuGlnVal	338
QY	969	TCACGCTCATTGGGGACCGGGAGATGACAGGCGCTGGGGTCACTCTGTGCCGACATC	1028
Db	339	SerArgSerIleGlyAspGlyGlnYsrYlsArgYsgGlyValaThrSerValProAspIle	358
QY	1029	AAGAAGCTCCAGCTGACCCCAATATGACAGGTTCAATTTTGTGGCTGTGATGGACTCTTC	1088
Db	359	ArgArgCysGlnLeuThrProAsnAspArgPheIleLeuLeuAlaCysAspGlyLeuPhe	378
QY	1089	AAGGCTTTTACCCCAAGAAAGCGCGGAATCTTACTGTGCTGTCTGAGAGATGAAGAAG	1148
Db	379	LeuValaPheThrProGlnGlnAlaValaAspPheIleLeuSerCysLeuGlnAspGlnYsr	398
QY	1149	ATTCAGACCGGGAGAGGAAGTCCGACGCGACGCGCCGCTGAAGAGAGCTGCACAG	1208
Db	399	IleGlnThrArgGlnGlyYsrSerAlaAlaAspAlaArgYsrGlnAlaAlaCysAsnArg	418
QY	1209	CTGGCGCAAGAGCGGTGACGGGGGCTCGCGCGACAAAGTCACTGATATGATGGTGGCGG	1268
Db	419	LeuAlaAsnYsrAlaValaGlnArgGlySerAlaAspAsnValaThrValaMetValaArg	438
QY	1269	ATAGGGCAC	1277

Db	Accession	Length	Score	Percent Similarity	Best Local Similarity	Query Match	Gap
Db	439	Illegal	441				
RESULT 3							
PCT-US01-01239-929							
Sequence 929, Application PC/TUS0101239							
GENERAL INFORMATION:							
APPLICANT: Human Genome Sciences, Inc., et al.							
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies							
FILE REFERENCE: PT213PCT							
CURRENT APPLICATION NUMBER: PCT/US01/01239							
CURRENT FILING DATE: 2001-01-17							
Prior application data removed - refer to PALM or file wrapper							
NUMBER OF SEQ. ID NOS: 2318							
SOFTWARE: PatentIn Ver. 2.0							
SEQ ID NO 929							
LENGTH: 446							
TYPE: PRT							
ORGANISM: Homo sapiens							
PCT-US01-01239-929							
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Pred. No.:	5,34e-171	Length:	446				
Score:	2199.00	Matches:	423				
Percent Similarity:	100.00%	Conservative:	0				
Best Local Similarity:	100.00%	Mismatch:	0				
Query Match:	85.90%	Indels:	0				
Gap:	1	Gaps:	0				
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QY	9	GGCCGCTGCTGCGCCGCGGGGTGTGAGCCGCGCGCTGCTGCGGGCTGAGTGTG	68				
DB	24	AlaAAGGCGCGAATGProGlyValTrpSerProAlaAlaAAGGlyLeuSerVal	43				
QY	69	TGTCCTGCTGCGGCTGCGCCGCGAGCTGCGCGAGACCTTGGCGGAGACCTGCGGAG	128				
DB	44	CysAAGGCGCGAATGProGlyValTrpSerProAlaAlaAAGGlyLeuSerVal	63				
QY	129	CCGAGGCTGCGCGGCGCGGCTGCGCGGAGAGAGCTGCGAGAGAGAGAGAGAGAGAG	188				
DB	64	ProGlyAAGGCTGCGGCGCGGCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG	83				
QY	189	GATGACCTGCTGCGCGAG	248				
DB	84	AspAAGGCTGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	103				
QY	249	GATGCTGCGAG	308				
DB	104	AspAAGGCTGCGAG	123				
QY	309	GTAAGGCTGCGAG	368				
DB	124	ValAAGGCTGCGAG	143				
QY	369	GAGAGCTGCGAG	428				
DB	144	GAGAGCTGCGAG	163				
QY	429	TATGCTGCGAG	488				
DB	164	TyrAAGGCTGCGAG	183				
QY	489	GATGCTGCGAG	548				
DB	184	AspAAGGCTGCGAG	203				
QY	549	GTTTGTGAG	608				
DB	204	ValAAGGCTGCGAG	223				
QY	609	AAGTGTGAG	668				

Db 224 AsnLeuIleArgLysPheProLysGlyAspValIleSerValGluYThrValLysArg 243
Qy 669 TGGCTTTGGACACTTCAAGCATCTGATGAAGATTCCTTAACAGCTTCACAG 728
Db 244 CysLeuLeuAspThrPheLysHisThrAspGluGlnPheLeuLysGlnIleAspSerGln 263
Qy 729 AAGCTGCTGGAAAGATGGGCTCACTGCCACGTGTGTTCTGGCTGTAAACAATTCTT 788
Db 264 LysProIleAlaTrpLysAspGlySerThrAlaThrCysValLeuAlaValAspAsnIleLeu 283
Qy 789 TATATTGGCAACCTGGAGATAGTGGGCAATCTTGTCGTTATATATAGAGAGATCA 848
Db 284 TyrIleAlaAsnLeuGlyAspSerArgAlaIleLeuCysArgGlyAsnGluLysSerGln 303
Qy 849 AAGCATGCAAGCTTAAGCTCAAGCAAGCATATCAACTCAGTATGAAGAGCGATG 908
Db 304 LysHisAlaAlaLeuSerLeuSerLysGluHisAsnProThrGlnTrpGluHisArgMet 323
Qy 909 AGGATTCAGAAAGGCTGGAGAAAGCTCAGGATGGCGGTGTTGGCGCTGTAAAGGTG 968
Db 324 ArgIleGlnLysAlaGlyAsnValArgAspGlyArgValLeuGlyValLeuGluVal 343
Qy 969 TCACGCTGCATTGGGGAGCGGGAGTCAAGCGCTGGGTGTCACTGTGCCCGGACATC 1028
Db 344 SerArgSerIleGlyAspGlyGlnTrpLysArgCysGlyValThrSerValProAspIle 363
Qy 1029 AGACGCTGCAGCTGACCCCAATGACAGGTTCAATTTGTGGCTGTATGGGCTCTTC 1088
Db 364 ArgArgCysGlnLeuThrProAsnAspArgPheIleLeuLeuAlaCysAspGlyLeuPhe 383
Qy 1089 AAGCTTTTACCCCAAGAAAGCTGGAATCTTCACTTGTCTGTCTGACAGATGAAGA 1148
Db 384 LysValPheThrProGluGluValAlaAsnPheIleLeuSerCysLeuGluAspGluLys 403
Qy 1149 ATCCAGACCCGGGAAGGAAGTCCGACGCCAGCGCCGTACAGAACACCTTCGACAG 1208
Db 404 ILeGlnThrArgGluGluLysSerAlaAlaAspAlaArgTrpGluAlaAlaCysAsnArg 423
Qy 1209 CTGGCCCAAGAGCGGTGACCGGGCTGGCGCGCAAGATCACTGATGTGTGGCGG 1268
Db 424 LeuAlaAsnLysAlaValGlnAspGlySerAlaAspAsnValThrValMetValAlaArg 443
Qy 1269 ATAGGGCAC 1277
Db 444 ILeGlyHis 446
RESULT 4
US-09-764-902-929
Sequence 929, Application US/09764902
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT213
CURRENT APPLICATION NUMBER: US/09/764,902
PRIORITY FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2318
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 929
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-902-929
Alignment Scores:
Pred. No.: 5,34e-171 Length: 446
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 403
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
DB: 21 Gaps: 0
US-09-935-124A-1 (1-1422) x US-09-764-902-929 (1-446)

Qy 9 GCCCGCTGTCGCGCCCGCGGGGTGTGAAGCCCGCGCTGCTCGCGGCTGAAGTGC 68
Db 24 AlaArgCysArgProProGlyValIlePheSerProAlaAlaIleArgGlyLeuSerVal 43
Qy 69 TGTGCTGTGCTGCGCTGCAACCCAGCTCCCGCATGACCTTTTGGGGACCTGCCGAG 128
Db 44 CysArgCysArgLeuHisProIleSerAlaMetAspLeuPheGlyAspLeuProGlu 63
Qy 129 CCCGAGCGTGGCGCGCGCGCTGCGGAAAGAAAGCTCAAGAAAGCAACCCCTGCTTT 188
Db 64 ProGluArgSerProAlaPheAlaValGluValAlaGlnLysGlyProLeuLeuPhe 83
Qy 189 GATGACCTCCCTCCGCGCAGAGTACTGACGATCAGGAGGAGCACTTTGCTTTTAT 248
Db 84 AspAspLeuProProIleSerSerThrAspSerGlySerGlyProLeuLeuPheAsn 103
Qy 249 GATCTCCCAACCGGCTAGCAGTGGCGATTCAGGTTCTTTGCCACATCAATCCAGATG 308
Db 104 AspLeuProProIleSerSerGlyAspSerGlySerLeuAlaThrSerIleSerGlnMet 123
Qy 309 GTAAAGACTGAAGGGAAGAGCAAGAAAGAAACCTCCGAGAAAGAGAGAAATGGCAGT 368
Db 124 ValLysTrpGluGlyLysGlyAlaLysArgLysTrpSerGluGluLysAsnGlySer 143
Qy 369 GAAGAGCTTGGAAGAAAGAAAGTTGTAAAGCTCTGCGTGAATCTTGTGCTGAAGGCG 428
Db 144 GluGluLeuValGluLysLysValCysLysAlaSerSerValIlePheGlyLeuLysGly 163
Qy 429 TATGTGCTGACGCGGAAGGGTGAAGGAGAGATGACAGATGCCACGTCACTGAAC 488
Db 164 TyrValAlaGluArgLysGlyGluArgGluGluMetGlnAspAlaHisValIleLeuAsn 183
Qy 489 GACATCACCGAGAGATGAAGGCGCCCATCGTCCCTTACCTCGGGGTTTCATATTGCT 548
Db 184 AspIleTrpGluGluCysArgProProSerSerLeuIleTrpValSerTrpPheAla 203
Qy 549 GTTTTGTGATGACATGAGAGAAATTCGACCTCAAAATTTGCTGACAGAAATTTGCATCA 608
Db 204 ValPheAspGlyHisGlyGlyIleArgAlaSerLysPheAlaAlaGlnAsnLeuHisGln 223
Qy 609 AACTTAATCAGAAATTTCTTAAGAGAGATGTATCACTGTAGAGAAACCGTGAAGAGA 668
Db 224 AsnLeuIleArgLysPheProLysGlyAspValIleSerValGluYThrValLysArg 243
Qy 669 TGGCTTTGGACACTTCAAGCATCTGATGAAGATTCCTTAACAGCTTCACAG 728
Db 244 CysLeuLeuAspThrPheLysHisThrAspGluGlnPheLeuLysGlnIleAspSerGln 263
Qy 729 AAGCTGCTGGAAAGATGGGCTCACTGCCACGTGTGTTCTGGCTGTAAACAATTCTT 788
Db 264 LysProIleAlaTrpLysAspGlySerThrAlaThrCysValLeuAlaValAspAsnIleLeu 283
Qy 789 TATATTGGCAACCTGGAGATAGTGGGCAATCTTGTCGTTATATATAGAGAGATCA 848
Db 284 TyrIleAlaAsnLeuGlyAspSerArgAlaIleLeuCysArgGlyAsnGluLysSerGln 303
Qy 849 AAGCATGCAAGCTTAAGCTCAAGCAAGCATATCAACTCAGTATGAAGAGCGATG 908
Db 304 LysHisAlaAlaLeuSerLeuSerLysGluHisAsnProThrGlnTrpGluHisArgMet 323
Qy 909 AGGATTCAGAAAGGCTGGAGAAAGCTCAGGATGGCGGTGTTGGCGCTGTAAAGGTG 968
Db 324 ArgIleGlnLysAlaGlyAsnValArgAspGlyArgValLeuGlyValLeuGluVal 343
Qy 969 TCACGCTGCATTGGGGAGCGGGAGTCAAGCGCTGGGTGTCACTGTGCCCGGACATC 1028
Db 344 SerArgSerIleGlyAspGlyGlnTrpLysArgCysGlyValThrSerValProAspIle 363
Qy 1029 AGACGCTGCAGCTGACCCCAATGACAGGTTCAATTTGTGGCTGTATGGGCTCTTC 1088
Db 364 ArgArgCysGlnLeuThrProAsnAspArgPheIleLeuLeuAlaCysAspGlyLeuPhe 383

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QY 1089 AAGGCTTTTACCCGAGAAAGCCGTGAATTGCTGCTGCTGAGAGTGAAG 1148
DB 384 LysValIlePheThrProGluGluValAlaIlePheIleLeuSerCysLeuGluIleAspGluLys 403
QY 1149 ATCCAGACCCCGGAGAGGAGTCCGACGCCGCCCTTACGAGACGCTTCGACAG 1208
DB 404 ILeGIlnThrArgGluGlyLysSerAlaIleAspAlaIleArgIleGluAlaIleCysAsnArg 423
QY 1209 CTGGCCAAACAAAGCGGTGTCAGCGGGGCTCGGCCGACAACTGACTGTGATGTGTGGG 1268
DB 424 LeuAlaAsnLysAlaIleValGlnArgGlySerAlaIleAspAsnValIleThrValMetValAlaArg 443
QY 1269 ATAGGCGAC 1277
DB 444 ILeGLYHis 446

RESULT 5
PCT-US01-03800A-2687
; Sequence 2687, Application PC/TUS0103800A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: PCT/US01/03800A
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO: 2687
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03800A-2687

Alignment Scores:
Pred. No.: 2,04e-166 Length: 421
Score: 2143.00 Matches: 414
Percent Similarity: 100.00% Conserved: 414
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.71% Indels: 0
Gaps: 0

US-09-935-124a-1 (1-1422) x PCT-US01-03800A-2687 (1-421)
QY 36 TGAAGCCCGGCGCTGCTGCTGCGGAGTGAAGTCTGCTGCTGCTGCGCTGCGCTGACCCAGCC 95
DB 8 TTPerProAlaIleAlaIleArgGlyLeuSerValCysArgCysArgLeuMetIleProAla 27
QY 96 TCGCCATGGAACCTCTTTCGGGAGCTGCGCGAGCCCGAGCGCTGCGCGCGCGCTGCC 155
DB 28 SerIleMetAspLeuPheGlyAspLeuProGluIleArgSerProAlaIleAla 47
QY 156 GGGAAAGAACTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCCGGCAGAGTACT 215
DB 48 GlyLysGluIleGlnLysGlyProLeuLeuPheAspAspLeuProProIleAspSerThr 67
QY 216 GACTCAGGATCAGGGGAGCCTTGTGCTTTGATGATCCCACTCCGCTAGCAGTGGCAT 275
DB 68 AsperGlySerGlyGlyProLeuLeuPheAspAspLeuProProIleAspSerGlyAsp 87
QY 276 TCAGGTTCTCTGCAATCATCATATCCAGATGTAAAGACTAAAGGAGAAAGAGCAAG 335
DB 88 SerGlySerIleuAlaIleThrSerIleSerGlnMetValLysThrGluGlyGlyAlaLys 107
QY 336 AGAAAAACCTCCAGAGAGAGAAAGAAATGCGAGTGAAGGTTGTGAAAAGAAAGTTGT 395
DB 108 ArgLysThrSerGluGluGluLysAsnGlySerGluIleuValGluIleLysValCys 127
QY 396 AAAGCTCTTCGGTGAATCTTGTGCTGAAGGCTATGTGCTGAGCGGAGGAGGAGAGG 455

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DB 128 LysAlaSerSerValIlePheGlyLeuLysGlyIleValAlaIleGluArgLysGlyGluArg 147
QY 456 GAGGAGATGCGAGAGGCCACGTCATCTGAGACGACATCACGAGAGTGTAGAGCCCA 515
DB 148 GluGluMetGlnAspAlaIleValIleLeuAsnAspIleThrGluGluCysArgProPro 167
QY 516 TCGTCCCTCATTAATCTCGGGTTTCATATTTGCTGTTTGTATGACATGAGAGAAATTCGA 575
DB 168 SerSerLeuIleThrArgValSerIlePheAlaIlePheAspGlyHisGlyGlyIleArg 187
QY 576 GCCTCAAAATTTGCTGCAAGAAATTTGCATCAAACTTAAACAGAAATTTCTTAAGA 635
DB 188 AlaSerLysPheAlaIleGlnAsnLeuIleGlnAsnLeuIleArgLysPheProLysGly 207
QY 636 GATGTAATCAGTGAAGAAAAACCTGAGAGAGATGCTCTTTGACATCTTCAAGCTACT 695
DB 208 AspValIleSerValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisIleThr 227
QY 696 GATGAAGATTCCTTAAACAGCTTCCAGCCAGAACCTGCTGGAAGATGGCTCCACT 755
DB 228 AspGluIlePheLeuLysGlnIleSerSerGlnLysProIleArgLysAspGlySerThr 247
QY 756 GCCACGATGTTCTGCTGTAGACAAATCTTATATTTGCCAACCTGAGATAGTCG 815
DB 248 AlaThrCysValIleuAlaValAspAsnIleLeuIleAlaIleAsnLeuGlyAspSerArg 267
QY 816 GCATCTGTGTGCTTATATATGAGAGAGTCAAAACATGACGCTTAAGCTCAGCAAA 875
DB 268 AlaIleLeuCysArgIleArgGlnIleSerGlnLysPheIleAlaIleLeuSerLeuSerLys 287
QY 876 GAGCATTAACCAATCAGTATGAAGAGCGATGAGATGACAGAAAGCTGAGAGAAAGTGC 935
DB 288 GluHisAsnProGlnGlnIleGluGluArgMetArgIleGlnLysAlaGlyGlyAsnVal 307
QY 936 AGGATGCGCGCTTTTGGCGCTGCTAGAGTGTCAAGCTCCATGAGGAGAGGCGCACTAC 995
DB 308 ArgAspGlyArgValIleuGlyValIleuGlnValSerIleSerIleLysAspGlyGlnIle 327
QY 996 AAGCGTCGCGGTGTCACCTGTGTGCGGACATGACAGCTGCCAGTCAACCCCAAGAC 1055
DB 348 ArgPheIleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGluGluAlaVal 367
QY 1116 AACTTCATCTTGTCTGCTGCGAGATGAAGATCCAGACCCGGAGAGGAGTCCGCA 1175
DB 368 AsnPheIleLeuSerCysLeuGluIleAspGluLysIleGlnThrArgGluGlyLysSerAla 387
QY 1176 GCCAGCGCCGCTAGAGACAGCTGCAAGAGCTGCGCAACAGCGGTGCGAGCGGCGC 1235
DB 388 AlaAspAlaArgIleGluAlaIleCysAsnArgLeuAlaAsnLysAlaValGlnArgGly 407
QY 1236 TCGGCCCAACAGTCACTGTATGTTGTTGCTGCGGATAGGCGAC 1277
DB 408 SerAlaAspAsnValIleThrValIleValArgIleGlyHis 421

RESULT 6
US-09-488-725A-5486
; Sequence 5486, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042

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Qy	1122	ATCTTGTCTGCTCTGAGAGAAAGAAATCCAGACCCGGGAGAGGAATCCGACGCCGAC	1183
Db	341	lileuueerCyaaeuuuaapduyyllegimhrzrgucluyyaserAlaalaap	360
Qy	1182	GCCGCTGACGACGAGCTTGACAGAGCTGCGCCAAACAGGCGGTGACAGGGGCTGCGCC	1241
Db	361	AlaArgrYrIduAlaAlaCyaaAmhrgrLsuAlaAmnyAlaAlaAlmhrgrLyserAla	380
Qy	1242	GACAACTGACCTGTGATGATGTGTGTCGGATAGGGCAC	1277
Db	381	AapaanvalThrValmeValValaIgrIlegIghIs	392
RESULT 8			
US-09-612-473-2			
Sequence 2, Application US/09612473			
GENERAL INFORMATION:			
APPLICANT: Bandman, Olga			
APPLICANT: Lal, Preeti			
APPLICANT: Hillman, Jennifer L.			
APPLICANT: Corley, Neil C.			
APPLICANT: Guebler, Karl J.			
APPLICANT: Shah, Purni			
TITLE OF INVENTION: HUMAN HYDROLASE- LIKE MOLECULES			
FILE REFERENCES: EP-04/00-1 CIP			
CURRENT APPLICATION NUMBER: US/09/612,473			
PRIOR FILING DATE: 2000-07-07			
PRIOR APPLICATION NUMBER: 09/013,881			
PRIOR FILING DATE: 1998-02-06			
NUMBER OF SEQ ID NOS: 55			
SOFTWARE: PERL Program			
SEQ ID NO 2			
LENGTH: 392.			
TYPE: PRT			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc feature			
OTHER INFORMATION: Incyte ID No: 195647			
US-09-612-473-2			
Alignment Scores:			
Pred. No.: 3,53e-156 Length: 392			
Score: 2018.00 Matches: 392			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 78.83% Indels: 0			
DB: 20 Gaps: 0			
US-09-935-124A-1 (1-1422) x US-09-612-473-2 (1-392)			
Qy	102	ATGAGACTCTTCGCGGAGACTGCGCGAGCCGACGCTGCGCCCGCTCGGCTCGGGAAA	161
Db	1	MeApAspLeuPnegIyAspLeuProGluProGluArgSerProAlaSerProAlaAlaGlyLys	20
Qy	162	GAAGCTCAGAAAGGACCCCTGCTCTTTGATGACTTCCTCCGCGACGACGACTGACTCA	221
Db	21	GlulAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer	40
Qy	222	GATCAGGAGGAGACTTTGCTTTTGTATGATCTCCACCCGCTAGCACTGCGATTCAGGT	281
Db	41	GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerLys	60
Qy	282	TCTCTTGCCACATCAATATCCACAGATGGTAAAGACTGAAGGAAAGGACGAAGGAAA	341
Db	61	SerLeuAlaThrSerLieserGlnMetValLysThrGluGlyLysGlyAlaLysArgLys	80
Qy	342	ACCTCGAGGAAGGAAAGAAATGAGCGTGAAGAGCTTGCGAAAAGAAAGTTGTGTAAGCC	401
Db	81	ThrSerGluGluGluLysAsnGlySerGluGluLeuValGluLysValCysLysAla	100
Qy	402	TCTTCGCGATCTTGGCTCGAAGGCGTAACTGTGCTGACCGGAAGGGGTGAGGGGAGAG	461
Db	101	SerSerValIlePheGlyLeuLysGlyValAlaGluArgLysGlyGluArgGluGlu	120

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Qy 462 ATGCAGATGCCGATCTCTGAAAGACATCACCGAGAGTGAAGCCCATCTGCC 521
    |||
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGlyAspGlyProPheSer 140
Qy 522 CTCATTACTCGGGTTTCATATTTTGTGTTTTGATGACATGAGAGATTCAGGCTCA 581
    |||
Db 141 LeuIleThrArgValSerGlyPheAlaValPheAspGlyHisGlyIleArgAlaSer 160
Qy 582 AATTTGTCGACAGAAATTTGCATCAAACTTAATGAGAAATTTCTTAAGAGATGTA 641
    |||
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
Qy 642 ATCAGCTGTAGAGAAACCGTGAAGAATGCTTTTGACACTTTCAAGCATCTGATGAA 701
    |||
Db 181 IleserValGluLysThrValLysAspGlyLeuLeuAspThrPheLysHisThrAspGlu 200
Qy 702 GAGTTCCTTAACAAAGCTTCCAGCGAGAGCTGCGTGAAGAAGATGGTCCATGCGCAG 761
    |||
Db 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaIleTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCTGTAGACAAACATTTTATATTCGCAACCTCGAGATAGTCCGGCATC 821
    |||
Db 221 CysValLeuAlaValAspAsnIleLeuTyrlleAlaAsnLeuGlyAspSerArgAlaIle 240
Qy 822 TTGTGCTGTTATATAGAGAGACTCAAAACATGACAGCTTAAAGCTTCAGCAAGAGCAT 881
    |||
Db 241 LeuGlyAspGlyAsnGluGlySerGlnLysHisAlaIleLeuSerLeuSerLysGluHis 260
Qy 882 AATCCAACTCAGATGAAGAGCGGATGAGAGATCAGAAGCTTGAGAGAAACCGCAGAGAT 941
    |||
Db 261 AsnProThrGlnTyrluGluAspMetArgIleGlnLysAlaGlyIleAsnValAlaArgAsp 280
Qy 942 GGGCGTGTGTTGGCGTGTAGAGAGTGTCAAGCTCCATTTGGGAGCGGAGATCAAGCCG 1001
    |||
Db 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyrluAspG 300
Qy 1002 TGGGCTGTCACCTCTGTGCCGACATCAACGCTGCCAGCTGACCCCAATGACAGATT 1061
    |||
Db 301 CysGlyValIleThrSerValProAspIleArgAspGlyGlnLeuThrProAsnAspArgPhe 320
Qy 1062 ATTTGTTGGCCGTGATGGGCTTCAGAGTCTTTATCCCGAAGAACCGCTGAACCTTC 1121
    |||
Db 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGluIleValAlaAsnPhe 340
Qy 1122 ATCTTGCTCTGCTCGAGAGTGAAGAATCCAGACCGGGAAGGAAGTCCGACGCGCAC 1181
    |||
Db 341 IleLeuSerCysLeuGluAspGlyLysIleGlnThrArgGluGlyLysSerAlaAlaAsp 360
Qy 1182 GCCCGCTACGAAGCAGCTTCGCAACAGGCTGGCCCAACAGGCGGTGACGCGGCTCGGCC 1241
    |||
Db 361 AlaArgTyrluAlaAlaCysAsnAspGlyLeuAlaAsnLysAlaValGlnArgGlySerAla 380
Qy 1242 GACAAGCTGATGATGATGGTGGTGGGATGAGGCAC 1277
    |||
Db 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 9
US-09-724-730-2
; Sequence 2: Application US/09724730
; GENERAL INFORMATION:
; APPLICANT: Hannigan, Gregory E.
; TITLE OF INVENTION: Novel Protein Phosphatase and Methods of
; FILE REFERENCE: KINE-016
; CURRENT APPLICATION NUMBER: US/09/724,730
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,225
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRN
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; ORGANISM: Homo sapiens
US-09-724-730-2

Alignment Scores:
Pred. No.: 3,536-156 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: 21 Gaps: 0

US-09-935-124a-1 (1-1422) x US-09-724-730-2 (1-392)

Qy 102 ATGACCTCTTCGGGAGACCTGCGGAGCCGAGCGCTGCGCGCCGCTGCGCGGAAA 161
    |||
Db 1 MetAspLeuPheGlyAspLeuProGluArgSerProAlaIleValLys 20
Qy 162 GAACTCAGAAAGACCCCTGCTTTGATGACCTCCGCGCCAGCATGACTCA 221
    |||
Db 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerThrAspSer 40
Qy 222 GGAATCAGGGGGACCTTGCTTTTGTATGATCTCCACCGCTAGCAGTGGCATTCAGGT 281
    |||
Db 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
Qy 282 TCTTTCGCACATCAATATCCAGATGTTAAAGACTGAAGGGAAGAGCAAGAGAAA 341
    |||
Db 61 SerLeuAlaIleThrSerIleSerGlnMetValLysThrGluGlyLysGlyAlaLysArgLys 80
Qy 342 ACCTCCAGAGAAAGAGAAATGGCAGTGAAGACTTTGTGGAAGAAAGAAAGTTTGTAAAGCC 401
    |||
Db 81 ThrSerGluGluGluLysAsnGlySerGluGluLeuValGluLysValCysLysAla 100
Qy 402 TCTTGCGATCTTTGCTGTAAGGGCTATGATGCTGAGCGTGAAGGAGGAGGAGGAG 461
    |||
Db 101 SerSerValIlePheGlyLeuLysGlyTyrluAlaGluLysGlyGlyGluArgGlu 120
Qy 462 ATGCAGATGCCAGTCACTGTAACGACATCACCGAGAGTGTAGGCCCATCTGCC 521
    |||
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProPheSer 140
Qy 522 CTCATTACTCGGGTTTCATATTTTGTGTTTTGATGACATGAGAGATTCAGGCTCA 581
    |||
Db 141 LeuIleThrArgValSerGlyPheAlaValPheAspGlyHisGlyIleArgAlaSer 160
Qy 582 AATTTGTCGACAGAAATTTGCATCAAACTTAATGAGAAATTTCTTAAGAGATGTA 641
    |||
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
Qy 642 ATCAGCTGTAGAGAAACCGTGAAGAATGCTTTTGACACTTTCAAGCATCTGATGAA 701
    |||
Db 181 IleserValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGlu 200
Qy 702 GAGTTCCTTAACAAAGCTTCCAGCGAGAGCTGCGTGAAGAAGATGGTCCATGCGCAG 761
    |||
Db 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaIleTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCTGTAGACAAACATTTTATATTCGCAACCTCGAGATAGTCCGGCATC 821
    |||
Db 221 CysValLeuAlaValAspAsnIleLeuTyrlleAlaAsnLeuGlyAspSerArgAlaIle 240
Qy 822 TTGTGCTGTTATATAGAGAGTCAAAACATGACAGCTTAAAGCTTCAGCAAGAGCAT 881
    |||
Db 241 LeuGlyAspGlyTyrluAsnGluGlySerGlnLysHisAlaAlaLeuSerLeuSerLysGluHis 260
Qy 882 AATCCAACTCAGATGAAGAGCGGATGAGATCAGAAGCTTGAGAGAAACGTCAGGAT 941
    |||
Db 261 AsnProThrGlnTyrluGluLysArgMetArgIleGlnLysAlaGlyIleAsnValAlaArgAsp 280
Qy 942 GGGCGTGTGTTGGCGTGTAGAGAGTGTCAAGCTCCATTTGGGAGCGGAGATCAAGCCG 1001
    |||
Db 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyrluAspG 300
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; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-124A-2

Alignment Scores:
Pred. No.: 3,53e-156 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: 23 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-935-124A-2 (1-392)

QY 102 ATGACCTCTTCGGGGACCTGCGGAGCCGAGCGCTGCGCGCGCCGGCTGCGGGGAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluArgSerProAlaIleGlyLys 20

QY 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCCGGCAGAGTACTGACTCA 221
DB 21 GluIleGlnLysGlyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 40

QY 222 GATCAGAGGGGACCTTTGCTTTTATGATCTCCACCCGCTAGCAGTGGCGATTGAGGT 281
DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProAlaSerSerGlyAspSerGly 60

QY 282 TCTCTGGCACATCAATATCCAGATGGTAAAGACTGAAAGGAAAGGCAAGGAA 341
DB 61 SerLeuAlaThrSerIleSerGlnMetValLysTrnGlnGlyLysGlyAlaLysArgLys 80

QY 342 ACCCTCGAGAGAGAGAGAGATGGCAGTGAAGACTTGTGAAAAGAAAGTTTGAAGCC 401
DB 81 ThrSerGlnGlnGlnLysAsnGlySerGlnLysValGlnLysValCysLysAla 100

QY 402 TCTTCGGTGAATTTTGGTCTGAAGGCTATGTGCTGACCGGAGAGGCTGAGGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyLysValAlaGlnArgLysGlyGlnArgGlnGln 120

QY 462 ATGACGATGCCACATGATCTCTGAACGACATCACCGAGATGAGCCCATCTGCC 521
DB 121 MetGlnAspAlaHisValIleLeuAsnAspIleTrnGlnGlnCysArgProProSerSer 140

QY 522 CTCATTACTCGGGTTTCATATTTCTGTTTGTGATGACATGAGGAATTCGACCTCA 581
DB 141 LeuIleThrArgValSerTrpPheAlaValPheAspGlnHisGlyGlyIleThrGlnAspSer 160

QY 582 AAATTGGTCGACAGAAATTTGCATCAAACTTAATCAGAAAATTTCTTAAGAGATGTA 641
DB 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180

QY 642 ATCAGTGAAGAAAACGCTGAAGAGATGCTTTTGGACACTTGAAGATCTGATGAA 701
DB 181 IleSerValGlnLysTrnValLysArgCysLeuLeuAspTrnPheLysHisTrnAspGln 200

QY 702 GAGTTCTCTTAAACAAAGCTTCCAGCAGAAAGCTGCTGAAAAGATGGGTCCACTCCACG 761
DB 201 GluPheLeuLysGlnAlaSerSerIleLysProAlaTrpLysAspGlySerThrLalaThr 220

QY 762 TGTGTTCTGGCTGTAGACAACATCTTTATATTTGCCAACCTCGAGATGATGGGCAATC 821
DB 221 CysValIleuAlaValAspAsnIleLeuTrpIleAlaAsnLeuGlyAspSerArgAlaIle 240

QY 822 TTGCTGCTTAAATAGAGAGAGTCAAAAACATGCACTTAAGCTTAAAGCTCAGCAAAAGCAT 881
DB 241 LeuCysArgLysArgGlnLysSerIleLysHisAlaAlaLeuSerLeuSerLysGlnHis 260

QY 882 AATCCAACTCAGTATGAGAGGCGATGAGATACAGAAAGCTGAGGAAACGTGAGGAT 941
DB 261 AsnProThrGlnTrpGlnGlnArgMetArgIleGlnLysAlaGlyLysValLysValArgAsp 280

QY 942 GGGCGTGTGGGGCTGAGAGGTGTCACGCTCATTTGGGAGCGGCAGTACAAGCGC 1001

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DB 281 GlyArgValIleGlnGlyValLeuGlnValSerArgSerIleGlyAspGlyGlnTrpLysArg 300

QY 1002 TGGGGTGCACCTCTGTGTCGCCGACATCAGACGCTGACGACCCCAATGACAGGTTC 1061
DB 301 CysGlyValIleThrSerValProAspIleLeuArgArgCysGlnLeuTrnProAsnAspArgPhe 320

QY 1062 ATTTTGTGGCCCTGTGATGGGCTCTTCAAGGTCTTTACCCGAGAAAGACCGTGAATTC 1121
DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheTrnProGlnGlnAlaValAsnPhe 340

QY 1122 ATCTTGTCTGTCTTCGAGAGTGAAGAAAGATCCAGACCCGGGAAAGGAATCCGACCCGAC 1181
DB 341 IleLeuSerCysLeuGlnAspGlnLysIleGlnTrnArgGlnGlyLysSerValAlaAsp 360

QY 1182 GCGGCTACAGAGCAGCTGCAACAGCGCTGACCAACAGAGCGGATGACGAGGCTCGGACC 1241
DB 361 AlaArgTrpGlnAlaAlaAlaCysAsnTrpLeuAlaAsnLysAlaValGlnArgGlySerAla 380

QY 1242 GACAACGTCACTGTGATGATGGTGGTGGGATAGGGCAC 1277
DB 381 AspAsnValTrnValMetValValArgIleGlyHis 392

RESULT 12
US-09-629-469A-10816
; Sequence 10816, Application US/09629469A
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/09/629, 469A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10816
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-629-469A-10816

Alignment Scores:
Pred. No.: 6,21e-156 Length: 392
Score: 2015.00 Matches: 391
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.74% Mismatches: 0
Query Match: 78.71% Indels: 0
DB: 20 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-629-469A-10816 (1-392)

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QY 102 ATGACCTCTTCGGGGACCTGCGGAGCCGAGGGCTGCGCGGGCCGGGCGGAAA 161
| | | | |
Db 1 MetAspLeuPheGlyAspLeuProGluPheGluThrGlySerProAlaIleGlyHis 20
| | | | |
QY 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCGCGGAGGTACTGATCA 221
| | | | |
Db 21 GluAlaGlnIlySerGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
| | | | |
QY 222 GGATCAGGGGAGACCTTTCCTTTTGATGATCTCCACCCGCTAGCGATGCGCATTCAGGT 281
| | | | |
Db 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
| | | | |
QY 282 TCTCTTGCACATCATATATCCAGATGTAAAGACTGAAAGGAGGAAAGCAAGAAA 341
| | | | |
Db 61 SerLeuAlaThrSerMetSerGlnMetValIlySerGluGluGlySerGlyAlaIlyAspGly 80
| | | | |
QY 342 ACCCTCCGAGAAAGAGAAATGCGAGTGAAGAGCTTGTGAAAAGAAAGTTTGTAAAGCC 401
| | | | |
Db 81 ThrSerGluGluGluIlySerGlnGlySerGluGluLeuValGluIlySerValCysIlySala 100
| | | | |
QY 402 TCTTGGGTGATCTTGGCTGGAAGGGGCTATGTGGCGGAGCGGAGGAGGAGAGAG 461
| | | | |
Db 101 SerSerValIlePheGlyLeuIlySerGlyTyValAlaGluIlySerGlyIlySerGluGlu 120
| | | | |
QY 462 ATGACGAGATGCCAGCTGATCTGTAAGACATCCAGAGAGTGTAGAGCCCGCATGTCC 521
| | | | |
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysIlySerProProSerSer 140
| | | | |
QY 522 CTCATTACTGGGCTTCAATTTTGTCTGCTTTTGTGATGACATGAGAGAAATTCAGGCTCA 581
| | | | |
Db 141 LeuIleThrValSerIlyPheAlaValIlePheAspGlyHisGlyIleHisGlyAlaSer 160
| | | | |
QY 582 AAATTTGCTGCAAGAAATTTGCATCAAACTTAATCAAGAAATTTCTTAAGAGATGTA 641
| | | | |
Db 161 LysPheAlaIleAlaGlnAsnLeuHisGlnAsnLeuIleAspIlySerPheIlySerValIle 180
| | | | |
QY 642 ATCAGTGTAGAGAAACCGTGAAGAGATGCCCTTTGAGACATTTCAACCATCTGATGAA 701
| | | | |
Db 181 IleSerValGluIlySerThrValIlySerValIlySerValIlySerValIlySerValIle 200
| | | | |
QY 702 GAGTTCCTTAAACAGACCTTCCAGCGAGAGGCTGCTGGAAGAGATGGTTCACCTGCAAG 761
| | | | |
Db 201 GluPheLeuIlySerGlnIlySerSerGlnIlySerProAlaIlySerIlySerThrAlaThr 220
| | | | |
QY 762 TGTCTGCTGTAGAGAAACATTTTATATTTGCCAACCTCGAGAGATGTGCGGCAATC 821
| | | | |
Db 221 CysValLeuAlaValAspAsnIleLeuIlyThrIleAlaAsnLeuGlyAspSerAlaIle 240
| | | | |
QY 822 TTGTGCTTATATAGAGAGTCAAAACATGAGCCTTAAGCCTTCAAGCAAGAGCAT 881
| | | | |
Db 241 LeuCysArgIlyAsnGlnIlySerGlnIlySerHisAlaIleAsnLeuSerIleSerGluHis 260
| | | | |
QY 882 AATCCAACTCATGATGAGAGGAGTGAAGATACAGAAAGCTGAGAGAAAGCTCAGGAT 941
| | | | |
Db 261 AsnProThrGlnIlySerGlnIlySerMetArgIleGlnIlySerAlaGlyIlySerValIlySer 280
| | | | |
QY 942 GGGCGTGTGTCGCTGCTAGAGGTGTCAAGCTTCATTTGGGAGCGGAGATCAAGCC 1001
| | | | |
Db 281 GlyArgValIleGlnIlyValIleGlnIlyValSerIlySerIleGlyAspIlyGlnIlySerArg 300
| | | | |
QY 1002 TGGCGTGTCACTCTGTGCGCGCATCAAGAGCTGCAAGCTGCAAGCTGCAAGAGGTTC 1061
| | | | |
Db 301 CysGlyValIleThrSerValIleProAspIleArgArgCysGlnIleuThrProAsnAspArgPhe 320
| | | | |
QY 1062 ATTTGTTGGCTGTGATGGGCTCTTCAAGGTCTTTACCCCAAGAAAGAGCCGTGAATTC 1121
| | | | |
Db 321 IleLeuLeuAlaCysAspGlyLeuPheIlySerValIlePheThrProGluGluIlyAlaIleAsn 340
| | | | |
QY 1122 ATCTTGTCTGTGCTCGAGAGTGAAGATCCAGAACCCGAGAGAGGAGATGCCAGCCGAC 1181
| | | | |
Db 341 IleLeuSerCysIleuGluAspGluIlySerIleGlnIlyThrArgGluGluIlySerSerAlaIleAsp 360
| | | | |

QY 1182 GCCCGCTACAGAGACCTTGGCAACGGCTGGCCAAAGAGCGGTGAGCGGGGCGGACC 1241
| | | | |
Db 361 AlaArgIlyGluAlaIleAlaCysAsnArgLeuAlaAsnIlyValAlaIleArgGlySerAla 380
| | | | |
QY 1242 GACAACGTCACTGTGATGTGTGTGCTGCGGATAGCGGAC 1277
| | | | |
Db 381 AspAsnValIleThrValMetValIleArgIleGlyHis 392
| | | | |
RESULT 13
US-09-488-725A-1914
; Sequence 1914, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784P/CT
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_FL_genes_b Versions 1.0
; SEQ ID NO 1914
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-1914
Alignment Scores:
Pred. No.: 7.5e-156 Length: 392
Score: 2014.00 Matches: 391
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.74% Mismatches: 0
Query Match: 78.67% Indels: 0
DB: Gaps: 0
US-09-935-124A-1 (1-1422) x US-09-488-725A-1914 (1-392)
QY 102 ATGACCTCTTCGGGAGACCTGCGGAGCCGAGGCTGCGCGGGCCGGGCGGAAA 161
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Db 1 MetAspLeuPheGlyAspLeuProGluPheGluThrGlySerProAlaIleGlyHis 20
| | | | |
QY 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCGCGGAGGTACTGATCA 221
| | | | |
Db 21 GluAlaGlnIlySerGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
| | | | |
QY 222 GGATCAGGGGAGACCTTTCCTTTTGATGATCTCCACCCGCTAGCGATGCGCATTCAGGT 281
| | | | |
Db 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
| | | | |
QY 282 TCTCTTGCACATCATATATCCAGATGTAAAGACTGAAAGGAGGAAAGCAAGAAA 341
| | | | |
Db 61 SerLeuAlaThrSerMetSerGlnMetValIlySerGluGluGlySerGlyAlaIlyAspGly 80
| | | | |
QY 342 ACCCTCCGAGAAAGAGAAATGCGAGTGAAGAGCTTGTGAAAAGAAAGTTTGTAAAGCC 401
| | | | |
Db 81 ThrSerGluGluGluIlySerGlnGlySerGluGluLeuValGluIlySerValCysIlySala 100
| | | | |
QY 402 TCTTGGGTGATCTTGGCTGGAAGGGGCTATGTGGCGGAGCGGAGGAGAGAG 461
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Db 101 SerSerValIlePheGlyLeuYleuYgLYrValAlaGluArgYleuYgLYuArgGluGlu 120
Qy 462 ATGCAGATGCCACGTCATCTCTGAACGACATCACCGAGAGGTGAGGCCCATCGTCC 521
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProIleProSer 140
Qy 522 CTCATTACTCGGGTTTCATATTTTGTCTGTTTGTATGACATGAGAGAAATCGAGCTCA 581
Db 141 LeuIleThrArgValSerTYrPheAlaValPheAspGlyHisGlyGlyIleArgAlaSer 160
Qy 582 AAATTGCTGCACAGAAATTTGATCAAACTTAATCAGAAATTTCTTAAGAGAGATGA 641
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysArgVal 180
Qy 642 ATCAGTGTAGAGAAAACCGTAAGAGATGCTTTTGGACACTTTCAGACATCTGATGA 701
Db 181 IleSerValGluLysThrValLysArgCysLeuLeuAspThrPheYleHisThrAspGlu 200
Qy 702 GAGTTCTTTAAACAGACTTCCAGCCAGAAAGCTGCTGGAAGATGGGTCCATCGCCAG 761
Db 201 GluPheLeuYgLYnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCGCTGAGACAACATCTTTATATTTGCCAAGCTGGAGATAGTGGCGCAATC 821
Db 221 CysValLeuAlaValAspAsnIleLeuYrIleAlaAsnLeuGlyAspSerArgAlaIle 240
Qy 822 TTGTCTCGTTATATGAGAGAGAGTCAAAAACATGACGCTTAAGCTTCAGCAAAAGACAT 881
Db 241 LeuCybArgTYrAsnGluLysSerGlnYleHisAlaAlaIleSerLeuSerYleuGlyHis 260
Qy 882 AATCCAACTCAGTATGAGAGCGGATGAGATACAGAAAGCTTGAAGAAAGCTCAGAGAT 941
Db 261 AsnProThrGlnTYrGluGluArgMetArgIleGlnLysAlaGlyLysAsnValArgAsp 280
Qy 942 GGGCGGTGTTGGGGGTGTAGAGGTGACCGTCCATTTGGGAGCGGAGATCAAGCC 1001
Db 281 GlyArgValLeuGlyValIleuGluValSerArgSerIleGlyAspGlyGlnTYrLysArg 300
Qy 1002 TGGCGTGTACCTCTGTGCGCCGACATCAGACGCTGCGACCTGACCCCAATGACAGTTT 1061
Db 301 CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
Qy 1062 ATTTGTGTGCGCTGTGATGGGCTTTCAAGGTCTTTACCCAGAAAGACGCTGAATCTT 1121
Db 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGluGluAlaValAsnPhe 340
Qy 1122 ATCTTGTCTCTGTGAGATGAAGATCCAGACCCGGGAGGGAAGTCCGACGCCGAC 1181
Db 341 IleLeuSerCysLeuGluAspGlyLysIleGlnThrArgGluGlyLysSerAlaAlaGln 360
Qy 1182 GCGCCCTACGAGACGCTGCAACAGGCTGGCCCAACAGGCGGTGCGAGCGGCTCGGCC 1241
Db 361 AlaArgTYrGluAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380
Qy 1242 GACAACTGCTGATGATGGTGTGCGGATAGGGGAC 1277
Db 381 AsnAsnValThrValMetValValArgIleGlyHis 392

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RESULT 14

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US-09-791-537-49417
; Sequence 49417, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49417

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; LENGTH: 392
; TYPE: PR
; ORGANISM: Rattus norvegicus
US-09-791-537-49417

Alignment Scores:
Pred. No.: 4,79e-149 Length: 392
Score: 1931.00 Matches: 373
Percent Similarity: 96.94% Conservative: 7
Best Local Similarity: 95.15% Mismatches: 12
Query Match: 75.43% Indels: 0
DB: 21 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-791-537-49417 (1-392)
Qy 102 ATGCAGCTTTCCGGGACCTGCGGAGCCGAGCGCTCGCGCGCGCGGCTGCGGAGAA 161
Db 1 MetAspLeuPheGlyAspLeuProGluProGluArgProProLysProSerAlaGlyLys 20
Qy 162 GAACTCAGAAAGAACCCCTGCTTTTGATGACTCCCTCCGCGCAGAGATGACTCA 221
Db 21 GlnAlaGlnGluGlyProValLeuPheGluAspLeuProProThrSerSerThrAspSer 40
Qy 222 GATCAGGGGAACTTTCCTTTTGATGATCTCCACCCGCTGACGAGTGGCGATTCAGGT 281
Db 41 GlySerGlyGlyProLeuLeuPheAspGlyLeuProProAlaGlySerGlyAsnSerGly 60
Qy 282 TCTCTGCGACATCAATATCCAGATGTTAAAGACTGAAGGGAAGAGCAAGAGAA 341
Db 61 SerLeuAlaThrSerGlySerGlnValLysAsnGluGlyLysGlyLysAlaLysArgLys 80
Qy 342 ACCCTCGAGAAAGAGAAATGCGACGTAGAGAGCTTGTGAAAGAAATTTGTAAAGCC 401
Db 81 AlaProGluGluGluLysAsnGlyGlyGluGluLeuValGluLysLysValCysLysAla 100
Qy 402 TCTTGGTGTATCTTGGTCTGAAGGCTATGTGCTGACCGGAGGCTGAGAGGAGAG 461
Db 101 SerSerValIlePheGlyLeuYleuYgLYrValAlaGluArgYleuYgLYuArgGluGlu 120
Qy 462 ATGCAGATGCCACGTCATCTCTGAACGACATCACCGAGAGGTGAGGCCCATCGTCC 521
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProIleProSer 140
Qy 522 CTCATTACTCGGGTTTCATATTTTGTCTGTTTGTATGACATGAGAGAAATCGAGCTCA 581
Db 141 LeuIleThrArgValSerTYrPheAlaValPheAspGlyHisGlyGlyIleArgAlaSer 160
Qy 582 AAATTGCTGCACAGAAATTTGATCAAACTTAATCAGAAATTTCTTAAGAGAGATGA 641
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysArgVal 180
Qy 642 ATCAGTGTAGAGAAAACCGTAAGAGATGCTTTTGGACACTTTCAGACATCTGATGA 701
Db 181 IleSerValGluLysThrValLysArgCysLeuLeuAspThrPheYleHisThrAspGlu 200
Qy 702 GAGTTCTTTAAACAGACTTCCAGCCAGAAAGCTGCTGGAAGATGGGTCCATCGCCAG 761
Db 201 GluPheLeuYgLYnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCGCTGAGACAACATCTTTATATTTGCCAAGCTGGAGATAGTGGCGCAATC 821
Db 221 CysValLeuAlaValAspAsnIleLeuYrIleAlaAsnLeuGlyAspSerArgAlaIle 240
Qy 822 TTGTCTCGTTATATGAGAGAGAGTCAAAAACATGACGCTTAAGCTTCAGCAAAAGACAT 881
Db 241 LeuCybArgTYrAsnGluLysSerGlnYleHisAlaAlaIleSerLeuSerYleuGlyHis 260
Qy 882 AATCCAACTCAGTATGAGAGCGGATGAGATACAGAAAGCTTGAAGAAAGCTCAGAGAT 941
Db 261 AsnProThrGlnTYrGluGluArgMetArgIleGlnLysAlaGlyLysAsnValArgAsp 280
Qy 942 GGGCGGTGTTGGGGGTGTAGAGGTGACCGTCCATTTGGGAGCGGAGATCAAGCC 1001

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Db 281 GIAYGValleuGIyValleuGIuValSerArserIleGIyAspGIyIntYrlyAsp 300
QY 1002 TCGGGTGCACCTCTGTGCCCCGACATCAGACCGCTGCCAGCTGACCCCAATGACAGTTCC 1061
Db 301 CySeGIyValThrSerValProAspIleArgArgCySeGInleuThrProAsnAspRhphe 320
QY 1062 ATTTTGTGGCCCTGTGATGGGCTCTTCAAGTCTTACCCCAAGAGAGCCGTGAATTC 1121
Db 321 IleleuLeuAlaCySeAspGIyLeuPheUyValPheThrProGIuGIuAlaValAsnPhe 340
QY 1122 ATCTGTCTGTCTCGAGATGAGAAAGATCCAGACCGGAGAGGAAAGTCCGACGGAC 1181
Db 341 IleleuSerCySeleuGIuAspGIuYsIleGIuThrArgIuGIuYsProAlaValAsp 360
QY 1182 GCGCGCTACGAGACGCTGCAAGCTGCGCAAGGCGGTGACGGGGCTCGGCC 1241
Db 361 AlAaRgYrGIuAlaAlaCySeAsnArgleuAlaAsnYsAlaValGIuAlaGIySerAla 380
QY 1242 GACAACTCACTGTGATGATGGTGGATGAGGCAC 1277
Db 381 AspaAsnValThrValMetValAlaArgIleGIyHis 392
RESULT 15
PCT-US02-25455-22
Sequence 22, Application PC/TUS0225455
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATION OF DARPP-32 PHOSPHORYLATION
FILE REFERENCE: 11181-005
CURRENT APPLICATION NUMBER: PCT/US02/25455
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,641
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 392
TYPE: PRT
ORGANISM: Rattus sp.
PCT-US02-25455-22
Alignment Scores:
Pred. No: 1 02e-148 Length: 392
Score: 1927.00 Matches: 372
Percent Similarity: 96.94% Conservative: 8
Best Local Similarity: 94.90% Mismatches: 12
Query Match: 75.27% Indels: 0
Gaps: 0
DB: 1
US-09-935-124A-1 (1-1422) x PCT-US02-25455-22 (1-392)
QY 102 ATGAGCCTCTTCGGGAGCCTGCCGAGCCGAGCGCTGCCGCCGCCGCTGCCGGGAAA 161
Db 1 MetAspLeuPheGIyAspLeuProGIuArgAlaProArgProSerAlaGIyHis 20
QY 162 GAACTCAGAAAGAGACCCCTGCTCTTGTATGACCTCCCTCCGCGCAGAGTACTGACTCA 221
Db 21 GIuAlaGIuGIuGIyProValIleuPheGIuAspLeuProThrSerSerThrAspSer 40
QY 222 GAATCAGGGGGACCTTTGCTTTTGTATGATCTCCACCGCTAGCAGTGGGCAATTCAGT 281
Db 41 GIySerGIyGIyProleuLeuPheAspGIyLeuProAlaIySerIyAsnSerGIy 60
QY 282 TCTCTTGCACATCATATCCCAAGTGTAAAGACTGAAGAGAAAGAGCAAGAGAAA 341
Db 61 SerleuAlaThrSerGIySerGIuValIyAsnGIuGIySerGIyAlaIyAspRlyS 80
QY 342 ACCCTCCGAGAGAGAAATGCGAGTGAAGGCTTGTGAGAAAAGAAATTTGTAAAGCC 401
Db 81 AlAaProGIuGIuGIuAspAsnGIyGIyGIuGIuValGIuIySerValCySylsAla 100
QY 402 TCTTGGTGATCTTTGTCTGAAGGGCTATGTGGCTAGCGGAGAGGTGAGGAGAG 461

Db 101 SerSerValIlePheGIyLeuYsGIyYrValAlaGIuArgIySeGIyGIuArgIuGIu 120
QY 462 ATTCAGATATGGCCCACTGCATCTCGAAGCAGCATCACCGAGAGGTGGGCCCACTGCTCC 521
Db 121 MetGIuAspAlaHisValIleleuAsnAspIleThrGIuGIuGIyAsnProProSerSer 140
QY 522 CTGATTAATCCGGTTCATATTTTGGCTTTTGAATGAGACATGAGAGAAATTCAGACTCA 581
Db 141 LeuIleThrArgValSerIyRheAlaValRheAspGIyHisGIyGIyIleArgAlaSer 160
QY 582 AAATTTGTCGACAGAAATTTGCTCAAACTTAATCAGAAAATTTCCCTAAAGAGATGA 641
Db 161 YsPheAlaAlaGIuAsnLeuHisGIuAsnLeuIleArgYsPheRouYsGIyAspVal 180
QY 642 ATCAGTGTAGAGAAAACCGTGAAGAGATGCTTTTGGACATTTCAAGCATATCTAGTGA 701
Db 181 IleSerValGIuYsThrValIyAspArgCySeleuAspThrPheYsHisThrAspGIu 200
QY 702 GAGTTCCTTAAACAAGCTTCACGACCAAGACCTGCTGAAAAGATGGGTCCACTGCCACG 761
Db 201 GIuPheLeuYsGIuAlaSerSerGIuYsProAlaTrpIyAspGIySerThrAlaThr 220
QY 762 TGTGTCTGCTGTGACACATCTTTATTTGCAACCTTCGAGATAGTGGGCAATC 821
Db 221 CyValleuAlaValAspAsnIleleuYrIleAlaAsnleuGIyAspSerArgAlaIle 240
QY 822 TTGTGCTTATATAGAGAGATCAAAAACATGACGCTTAAGCTTCAGCAAAAGCAT 881
Db 241 LeuCyArgIyArgIuGIuSerGIuYsHisAlaIleleuSerIySeGIyHis 260
QY 882 AATTCAACTCATATGAGAGCGGATGAGAGATGACAGAGCGTGGAGAGAACTCAGAGAT 941
Db 261 AsnProThrGIuYsGIuGIuArgMetArgIleGIuYsAlaGIyGIyAsnValArgAsp 280
QY 942 GGGCGGTGTTGGCGCTGCTGAGAGTGCAGCTGCATTTGGGAGCGGAGTCAAGCGC 1001
Db 281 GIyArgValleuGIyValleuGIuValSerArgSeIleGIyAspGIyIntYrlyAsp 300
QY 1002 TCGGTGTACCTCTGTGCCGACATCAGACGCTGCCAGCTGACCCCAATGACAGTTTC 1061
Db 301 CySeGIyValThrSerValProAspIleArgArgCySeGInleuThrProAsnAspRhphe 320
QY 1062 ATTTTGTGGCCCTGTGATGGGCTCTTCAAGTCTTACCCCAAGAGAGCCGTGAATTC 1121
Db 321 IleleuSerCySeleuGIuAspGIuYsIleGIuThrArgIuGIuYsProAlaValAsp 340
QY 1122 ATCTGTCTGTCTCGAGATGAGAAAGATCCAGACCGGAGAGGAAAGTCCGACGGAC 1181
Db 341 IleleuSerCySeleuGIuAspGIuYsIleGIuThrArgIuGIuYsProAlaValAsp 360
QY 1182 GCGCGCTACGAGACGCTGCAAGCTGCGCAAGGCGGTGACGGGGCTCGGCC 1241
Db 361 AlAaRgYrGIuAlaAlaCySeAsnArgleuAlaAsnYsAlaValGIuAlaGIySerAla 380
QY 1242 GACAACTCACTGTGATGATGGTGGATGAGGCAC 1277
Db 381 AspaAsnValThrValMetValAlaArgIleGIyHis 392
RESULT 16
US-10-218-137-22
Sequence 22, Application US/10218137
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Svenningsen, Per
APPLICANT: Rakhilin, Sergey
APPLICANT: Starkova, Natalia
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATION OF DARPP-32 PHOSPHORYLATION
FILE REFERENCE: 11181-005
CURRENT APPLICATION NUMBER: US/10/218,137
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,641
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 23

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-218-137-22

Alignment Scores:
Pred. No.: 1,02e-148 Length: 392
Score: 1927.00 Matches: 372
Percent Similarity: 96.94% Conservative: 8
Best Local Similarity: 94.90% Mismatches: 12
Query Match: 75.27% Indels: 0
DB: Gaps: 0

US-09-935-124A-1 (1-1422) x US-10-218-137-22 (1-392)

QY 102 ATGACACCTTTGGGGGACCTGCGGAGCCGCTCCGCGCGCGCGCTGCGCGGAAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluArgAlaProArgProSerAlaGlyLys 20
QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCCGCGCAGTACTGACTCA 221
DB 21 GluAlaGlnGlnGlyProValLeuPheGluAspLeuProThrSerSerThrAspSer 40
QY 222 GGATCAGGGGACCTTTGCTTTTGTATGATCTCCACCCGCTAGCAGTGCATTCAGGT 281
DB 41 GlySerGlyGlyProLeuLeuPheAspGlyLeuProProAlaGlySerGlyAsnSerGly 60
QY 282 TCTCTTGGCCACATCATATCCCGATGCTTAAAGCTGAAAGGAAAGACCAAGAAAA 341
DB 61 SerLeuAlaThrSerGlySerGlnValLysAsnGlnGlySerGlyAlaLysArgLys 80
QY 342 ACCTCCGAGAAAGAAAGATGGCAGTGAAGAGCTTGTAAGAAAGAAAGTTTGAAGGC 401
DB 81 AlaProGlnGlnGlnAspAsnGlnGlyGlnGlnLeuValGlnLysLysValCysLysAla 100
QY 402 TCTTGGGTATCTTTGGTGTGAAGGGCTATGTGGCTGAGCGGAAGGGTGAAGGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyLysArgGln 120
QY 462 ATGCAGAGATGCCACCTCATCTGAAACGACATCACCGAGAGTGTAGGCCCATGTGTC 521
DB 121 MetGlnAspAlaIleValIleLeuAsnAspIleThrGlnGlnCysAsnProProSerSer 140
QY 522 CTCATTAATCCGGGTTTCATATTTTGTGTTTGTATGATGACATGAGAGAAATTGAGCCTCA 581
DB 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyIleArgAlaSer 160
QY 582 AAATTGTCTGACAGAAATTGACATAAACTTAATCAGAAAAATTTCTTAAGGAGATGTA 641
DB 161 LysPheAlaIleGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
QY 642 ATCAGTGTGAAGAAAACGCTGAAGAGATGCTTTTGGACATTTCAAGCATACTGATGAA 701
DB 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGln 200
QY 702 GAGTTCCTTAAACAGCTTCCAGCGCAGAGCGCTGAAAGATGGGTCCACTGCGCAG 761
DB 201 GluPheLeuLysGlnIleAspSerGlnLysProAlaTyrLysAspLysSerThrAlaThr 220
QY 762 TGTGTCTTGGCTGTAGACAAACATTTCTTTATTTGCAACCTCGAGATAGTGGCAATC 821
DB 221 CysValIleLeuAlaValAspAsnIleLeuTyrIleAlaAsnLeuGlnLysPheArgAlaIle 240
QY 822 TTGTGTCTTATATGAGAGAGTCAAAAACATGACGCTTAAAGCTTACGCAAAAGCAT 881
DB 241 LeuCysArgTyrAsnGlnLysSerGlnLysHisAlaIleLeuSerLeuSerLysGlnHis 260
QY 882 AATCCAACTCAGATGAAGAGCGGATGAGGATACAGAAGCTGAGAGAAACGTCAGGGAT 941
DB 261 AsnProThrGlnTyrGlnLysArgMetArgIleGlnLysAlaGlyGlyAsnValArgAsp 280
```

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QY 942 GGGCGTGTGTTGGCGCTGTACAGGTGTACAGCTCCATTTGGGGACGGGAGTACAGCGC 1001
DB 281 GlyArgValIleuGlyValLeuGlnValSerArgSerIleGlyAspGlyGlnTyrLysArg 300
QY 1002 TGGCGGTGCACCTCTGTGTGTCGAGATCAGACGCTCCGAGCTGAGCCCAATGACAGTTTC 1061
DB 301 CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
QY 1062 ATTTGTGTCCTGTGATGAGGCTCTTCAAGGTCTTTACCCGAGAAAGACCGTGAATTC 1121
DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGlnLysAlaValAsnPhe 340
QY 1122 ATCTTGCTCTGTCTGAGAGTGAAGAAATCCAGACCCGGGAAAGGAGATCCGACCGAC 1181
DB 341 IleLeuSerCysLeuGlnAspGlnLysIleGlnThrArgGlnGlyLysProAlaValAsp 360
QY 1182 GCCCGCTACGAGCAGCCTGCAACAGCTGCGCACAAGCGCGTGCACCGGGCGTCCGCC 1241
DB 361 AlaArgTyrGlnAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380
QY 1242 GACAAGTCACTGTGATGATGGTGGCGGATAGGGCAC 1277
DB 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 17
US-60-245-228-374
; Sequence 374, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; FILE REFERENCE: C1000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HUMAN
US-60-245-228-374

Alignment Scores:
Pred. No.: 2.63e-146 Length: 373
Score: 1897.50 Matches: 373
Percent Similarity: 95.15% Conservative: 0
Best Local Similarity: 95.15% Mismatches: 0
Query Match: 74.12% Indels: 19
DB: Gaps: 1

US-09-935-124A-1 (1-1422) x US-60-245-228-374 (1-373)

QY 102 ATGACACCTTTGGGGGACCTGCGGAGCCGCTGCGCGCGCGCTGCGCGGAAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluArgSerProArgProAlaIleGlyLys 20
QY 162 GAAGTCAAGAAAGAACCCCTGCTTTGATGACCTCCCTCCGCGCAGTACTGACTCA 221
DB 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThr----- 38
QY 222 GGATCAGGGGACCTTTGCTTTTGTATGATCTCCACCCGCTAGCAGTGCATTCAGGT 281
DB 39 -----AspSerGly 41
QY 282 TCTCTTGGCCACATCAATATCCAGATGTGAAGACTGAAGGAAAGGAAAGGAAAGAAA 341
DB 42 SerLeuAlaThrSerIleSerGlnMetValLysThrGlnGlnGlyLysGlyAlaLysArgLys 61
QY 342 ACCTCCGAGAAAGAAAGAAATGCGCAGTGAAGCTTTGTGAAAGAAAGAAAGTTTGAAGGC 401
DB 62 ThrSerGlnGlnGlnLysAsnGlySerGlnGlnLysValGlnLysLysValCysLysAla 81
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[illegible]

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Db 222 G1yAaGValleuG1yValleuG1yValSerArgSer1leG1yAspG1yGlnTyryLysArg 241
Qy 1002 TCGGCTGTCACCTCTGTGCCCCGACATCAAGCTGCGACCTGACCCCGACATGACAGGTTTC 1061
Db 242 CySG1yValThSerValProAsp1leArg1yGySG1nLeuThrProAsnAspArgPhe 261
Qy 1062 ATTTGTTGGCTGTGATGGGCTCTTCAAGTCTTTTACCCGAGAAAGCCCGTGAACCTTC 1121
Db 262 1leuLeuAla1CyAspG1yLeuPhe1yValPheThrProG1nG1nAlaValAsnPhe 281
Qy 1122 ATCTTGCTGTCTGAGATGAAAGATCCAGACCCCGGAAAGGAAAGTCCGAGCCGAC 1181
Db 282 1leuLeuSerCyLeuG1nAspG1yLys1leG1nThrArgG1nG1yLysSer1Ala1Asp 301
Qy 1182 GCCCGCTACGAAGACGCTGCAACAGGCTGCGCAACAAAGCGGCTGACGGGCTCGGCC 1241
Db 302 AlaArgTyG1nAla1Ala1CyAsnAsnArgLeuAlaAsn1yAlaValG1nArgG1ySer1Ala 321
Qy 1242 GACAACTGACTGTGATGGTGTGGCGGATAGGGCAC 1277
Db 322 AspaenValThrValMetValValArg1leG1yHis 333

RESULT 19
US-60-229-518-348
; Sequence 348, Application US/60229518
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000778
; CURRENT APPLICATION NUMBER: US/60/229,518
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 333
; TYPE: PRT
; ORGANISM: HUMAN
US-60-229-518-348

Alignment Scores:
Pred. No.: 1,296-128 Length: 333
Score: 1681.50 Matches: 333
Percent Similarity: 84.95% Conservatve: 0
Best Local Similarity: 84.95% Mismatches: 0
Query Match: 65.68% Indels: 59
Db: 27 Gaps: 1

US-09-935-124a-1 (1-1422) x US-60-229-518-348 (1-333)
Qy 102 ATGACCTTGTGGGGAGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAAA 161
Db 1 MetAspLeuPheG1yAspLeuProG1nArgSerProArgProAla1leG1yLys 20
Qy 162 GAAGCTCAAGAAAGACCCCTGCTTTTGATGACCTCCCTCCGCGACAGACTGACTCA 221
Db 21 G1uAlaG1nLysG1yProLeuLeuPheAspLeuProProAla1leSerThrAspSer 40
Qy 222 GATCAGGGGACCTTGTCTTTTGATGATCTCCACCCGCTAGACAGTGGCGATTCAGGT 281
Db 40 ----- 40
Qy 282 TCTCTTGCACATCAATATCCAGATGTAAAGACTGAAGGAAAGAGAAAGAGAAA 341
Db 40 ----- 40
Qy 342 ACCTCCGAGAGAGAGAGAAATGACAGTGAAGACTTGTGAAAGAAAGTGTAAAGCC 401
Db 41 -----Ala 41
Qy 402 TCTTGGTGATCTTTGTCTGTGAAGGCTATGTGCTGACGGAAGGCTGAGAGGAGAG 461

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Db 42 SerSerVal1lePheG1yLeuLysG1yTyryValAlaG1nArg1yG1nArgG1nG1n 61
Qy 462 ATGACAGATGCCACGATCACTCTGAACGACATCACCGAGATGATAGGCCCATCGTCC 521
Db 62 MetG1nAspAla1nVal1leuLeuAsnAsp1leThrG1nG1nG1nG1nG1nG1nG1nG1n 81
Qy 522 CTGATTAAGCTGGGTTTCATATTTTCTGTTTGTGATGACATGAGAGAAATTCAGCCTCA 581
Db 82 Leu1leThrArgValSerTyryrPheAlaValPheAspG1yHisG1yG1y1leArg1leSer 101
Qy 582 AAATTTGCTGCACAGAAATTTGATCAAAACTTAATCAGAAATTTCTTAAGAGATGTA 641
Db 102 LysPheAla1AlaG1nAsnLeu1leG1nAsnLeu1leArg1yPheProLysG1yAspVal 121
Qy 642 ATCAGTGTAGAGAAACCGTGAAGAGATGCCCTTTTGAACCTTGAACATTCATGATGA 701
Db 122 1leSerValG1nLysThrValLysArgCyLeuLeuAspThrPheLysHisThrAspG1n 141
Qy 702 GAGTTCCTTAAACAACTTCCAGCCAGAACCTGCTGGAAGATGGTCCACTGCCACG 761
Db 142 G1uPheLeuLysG1nAla1leSerSerG1nLysProAla1leP1yAspG1ySerThrAlaThr 161
Qy 762 TGTGTTCTGGCTGTGACAACTTTTATATTCGCAACCTCGAGATATGTCGGGCATC 821
Db 162 CySVal1leuAlaValAspAsn1leuTyry1leAlaAsnLeuG1yAspSerArgAla1le 181
Qy 822 TTGTGCTGTTAATGAGAGAGATCAAAACATGAGGCTTAAGCTCAGCAAAAGAGAT 881
Db 182 LeuCyAsArgTyryrAsnG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1n 201
Qy 882 AATCCAACTCAATATGAAGCGGATGAGATACAGAAAGCTGAGAGAAACCTCAGGAGAT 941
Db 202 AsnProThrG1nTyryG1nG1nArgMetArg1leG1nLysAlaG1yLysValArgAsp 221
Qy 942 GGGCTGTTTGGGCTGTGAGGTGTCAGGCTCACTGAGGAGCGGAGATGACAGCGC 1001
Db 222 G1yAaGValleuG1yValleuG1yValSerArgSer1leG1yAspG1yGlnTyryLysArg 241
Qy 1002 TCGGCTGTCACCTCTGTGCGCGACATGACGCTGCGACCGCGCGCGCGCGCGCGCGCGG 1061
Db 242 CySG1yValThSerValProAsp1leArg1yGySG1nLeuThrProAsnAspArgPhe 261
Qy 1062 ATTTGTTGGCTGTGATGGGCTCTTCAAGTCTTTTACCCGAGAAAGCCCGTGAACCTTC 1121
Db 262 1leuLeuAla1CyAspG1yLeuPhe1yValPheThrProG1nG1nAlaValAsnPhe 281
Qy 1122 ATCTTGCTGTCTGAGATGAAAGATCCAGACCCCGGAAAGGAAAGTCCGAGCCGAC 1181
Db 282 1leuLeuSerCyLeuG1nAspG1yLys1leG1nThrArgG1nG1yLysSer1Ala1Asp 301
Qy 1182 GCCCGCTACGAAGACGCTGCAACAGGCTGCGCAACAAAGCGGCTGACGGGCTCGGCC 1241
Db 302 AlaArgTyG1nAla1Ala1CyAsnAsnArgLeuAlaAsn1yAlaValG1nArgG1ySer1Ala 321
Qy 1242 GACAACTGACTGTGATGGTGTGGCGGATAGGGCAC 1277
Db 322 AspaenValThrValMetValValArg1leG1yHis 333

RESULT 20
PCT-US01-08631-40296
; Sequence 40296, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736

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Db 115SerValGluIyThrValIySarGyLeuLeuAspThrPheYshArTrAbpGlu 60
Qy 702 GAGTTCCTTAAACAAAGCTTCACAGCAAGCCCTGCGAAGATGGGTCCATGCGACG 761
Db 61 GluPheLeuIySglInIaSerSerGlnIyPheAlaTrPlyAspIySerThrAlaThr 80
Qy 762 TGTGTTCTGGCTGTAGACAACATCTTTATATTGCAACCTCGAGATAGTCGGGCAATC 821
Db 81 CyValIleuAlaValIAspEnIleuTyrlLeAlaAsnIleuIyAspSerArGAlaIle 100
Qy 822 TTGTGTCCTTAAATAGAGAGACTCAAAAATGCAAGCCTTAAGCCTCAAGCAAGAGCAT 881
Db 101 LeuCyArGlyTrAsnGluIySerGlnIyShIAlaAlaLeuSerLeuSerIySgluHs 120
Qy 882 AATCCAACTCAGTATGAAGAGCGATGAGATACAGAAAGGCTGAGAAAACGTCAAGGAT 941
Db 121 AsnProThGlnIyrluGluIyAspMetArGIlleGlnIyAlaIyAlaIyAsnValArGAsp 140
Qy 942 GGGCGGTGTTGGGCGTGTAGAGGTGTCACGCTCCATTGGGAGCGGCGAGTACAAAGCGC 1001
Db 141 GluArGValIleuGlyValIleuGluValSerArGSerIleGlyAspGlyGlnIyrluSarG 160
Qy 1002 TGGCGGTGTCACCTCTGTGCGCCGACATCAAGCTGCCAGCTGAACCCCAATGACAGTTTC 1061
Db 161 CySgIyValThrSerValIProAspIleArGArGySgIleuThrProAsnAspArGpHe 180
Qy 1062 ATTTGTTGGCCTGTATGGGCTCTTCAAGGTCTTTACCCAGAAAGCGGGAATTC 1121
Db 181 IleLeuLeuAlaCyAspIyIleuPheIyValIlePheThrProIuGluAlaValAspHe 200
Qy 1122 ATCTGTCTGTCTCGAGATGAAAATTCAGACCCCGGAGAGGAAGTCCGACGCGAC 1181
Db 201 IleLeuSerCyLeuGluIyAspGluIyIleGlnThrArGluIyIySerAlaIaAsp 220
Qy 1182 GCGCGGTAGAGAGACCTTCGCAACAGCTGGCCAAACAAGCGGTGCGAGCGGCTCGGCC 1241
Db 221 AAlArGlyrluAlaIaCyAsnArGLeuAlaAsnIySAlaValGlnArGlySerAla 240
Qy 1242 GACAACGTCACTGTATGGTGTG 1265
Db 241 AspAsnValThrValMetValVal 248

RESULT 22
PCT-US01-08631-40295
; Sequence 40295, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40295
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (184)..(194)
; OTHER INFORMATION: Protein phosphatase 2C proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number B101032C, p-value=3.195e-12, raw score of 6.14
; LOCATION: (144)..(211)
; OTHER INFORMATION: Protein phosphatase 2C domain identified by Pfam, accession
; OTHER INFORMATION: name PP2C, E-value=9.2e-09, Pfam score of 34.3
PCT-US01-08631-40295
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Alignment Scores:
Pred. No.: 3,77e-77 Length: 221
Score: 1053.00 Matches: 206
Percent Similarity: 96.26% Conservative: 0
Best Local Similarity: 96.26% Mismatches: 0
Query Match: 41.13% Indels: 8
DB: 1 Gaps: 1

US-09-935-124A-1 (1-1422) x PCT-US01-08631-40295 (1-221)
Qy 36 TGGAGCCCGGCGCGCTGCTCGCGGCGTGAAGTGTCTGCTGCTGCGGCTCCAGCCAGCC 95
Db 8 TrpSerProAlaAlaIaArGlyIyLeuSerValCySarGyCySarGluHsIProAla 27
Qy 96 TCCGCCATGACCTCTTCGGGAGCTGCGCGAGCCCGAGCGCTCGCGCGCGCGCTGCGC 155
Db 28 SerAlaMetAspLeuPheGlyAspLeuProGluProGluArGSerProArGProAlaIa 47
Qy 156 GGGAAAAGAGCTCAGAAAGAGACCCCTGCTTTGATGACTTCCTCCGCGCAGCACTACT 215
Db 48 GlySgIyAlaGlnIyGlyIyProLeuLeuPheAspAspLeuProAlaSerSerThr 67
Qy 216 GACTCA-----GGATCAGGGGAGCCTTGGTTTGTATGAT 251
Db 68 AspSerGlySerSerIleuGlnAlaLeuProGlySerGlyIyProLeuLeuPheAspAsp 87
Qy 252 CTCCACCCGCTAGAGAGTGGCGATTCAGGTTCTTGGCACTACATATCCAGATGTGA 311
Db 88 LeuProProAlaSerSerIyAspSerGlySerIleuAlaThrSerIleSerIleMetVal 107
Qy 312 AAGACTGAAGGGAAGAGCAAAAGAAAACCTCCGAGAAAGAGAAGATGGCAGTGA 371
Db 108 IySthrGluGlyIyGlyIyAlaIySarGlySthrSerGluGluIyIyAsnGlySerGlu 127
Qy 372 GAGCTTGGGAAAGAAAGTTGTAAAGCTTGGGAGTGTGGTGTGCTGAAGGCTAT 431
Db 128 GluLeuValGluIyIyValIyCySlyAspAspSerValIlePheGlyIyLeuIySglYly 147
Qy 432 GTGCGTGAAGCGGAGGTGAGAGAGAGAGATGACAGATGCCACGTATCCTGAAGCAG 491
Db 148 ValAlaGluArGlyGlyIyGluArGlyGluIyMetGlnAspAlaIleValIleuAsnAsp 167
Qy 492 ATCACCAGAGAGTGAAGCCCATGCTGCTCATTTACTCGGGTTTCATATTTTGTGTT 551
Db 168 IleThrGluGluCyArGProProSerSerIleuIleThrArGValSerIyPheAlaVal 187
Qy 552 TTTGATGACATGAGAGAAATTCGAGCTCAAAATTTGCTGCAACAATTTGATCAAAAAC 611
Db 188 PheAspGlyHsIySgIyIleArGAlaSerIySPhenAlaAlaGlnAsnIySglnAsn 207
Qy 612 TTAATCAGAAATTTCTTAAAGAGATGTAAATCACTGTAGAG 653
Db 208 LeuIleArGlySPhenProIySgIyAspValIleSerValGlu 221

RESULT 23
US-09-791-537-134656
; Sequence 134656, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134656
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-134656
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Alignment Scores:

Pred. No.:	4,81e-61	Length:	167
Score:	956.00	Matches:	165
Percent Similarity:	99.40%	Conservative:	1
Best Local Similarity:	98.80%	Mismatches:	1
Query Match:	33.44%	Indels:	0
DB:	21	Gaps:	0

US-09-935-124a-1 (1-1422) x US-09-791-537-134656 (1-167)

QY 570 ATTGAGCCTCAAAATTGTCGACAGAAATTGCACTTAAATTCAGAAAATTTCT 629

DB 1 TLeTgAlAserLyLeuAlaAGInAsenLeuH1sgInAsenLeuH1eArGlySPhenPro 20

QY 630 AAAGAGATGTATCATAGTGTAGAGAAAACCGTGAAGAGATGCTTTTGAACACTTCAAG 689

DB 21 LyeGlyAspLleIleSeVaIGluYerThValYsArGySbleuLeuAspThrPheLyS 40

QY 690 CATACTGATGAAGATTCTTAAACAAAGCTTCCAGCAGAGAGCTGCTGGAAGATGGG 749

DB 41 H1eThrAspGluGluPheLeuLyGlnAlAserSerGlnLySProAlaTrpLyAspGly 60

QY 750 TCCATGCGCAGGTGTGTTCTGCTGTAGACAACATCTTATATTCGCAACCTCGAGAT 809

DB 61 SerThAlaThrCyValLeuAlaValAspAsnLleuYrLleAlaAsenLeuGlyAsp 80

QY 810 AGTCGGGCAATCTGTGCTGTATATGAGAGAGAGCAAAAACATGAGAGCTTAAAGCTC 869

DB 81 SerTgAlaIleLeuCyAspGlyTAsnGluGluSerGlnLySPhenAlaAlaLeuSerLeu 100

QY 870 AGCAAGAGCATTAATCCACTCATATGAAAGCCGATAGAGATPAGAAAGGCTGAGGA 929

DB 101 SerLySglnH1AsnProThrGlnYrGluGluAspMetCAsGlnLySAlaGlyGly 120

QY 930 AACGTACGAGATGGCGCTGTTTGGCGCTCTAGAGGTCAAGCTCCATTGGGAGCGG 989

DB 121 AsnValArAspGlyArValLeuGlnValLeuGlnValSerAspSerLleGlyAspGly 140

QY 990 CAGTACAGCGCTGCGGTGTCACTCTGTGCTCCGACATGAGCGCTGCACTGACCCCC 1049

DB 141 GlnTrLyArArCySgLyValThSerValProAspLleArGArCySglnLeuThrPro 160

QY 1050 AATGACAGGTTCATTGTTGTTG 1070

DB 161 AsnAspArpPheIleLeuLeu 167

RESULT 24

US-09-834-366-15305 Application US/09834366

GENERAL INFORMATION:

APPLICANT: Benjamin, Stephanie

APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Yves

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: 81 US2 REG

CURRENT APPLICATION NUMBER: US/09/834,366

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: US 60/197,873

PRIOR FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 52153

SOFTWARE: Patent.pm

SEQ ID NO 15305

LENGTH: 123

TYPE: PRT

ORGANISM: Homo sapiens

US-09-834-366-15305

Alignment Scores:

Pred. No.:	2.56e-42	Length:	123
Score:	627.00 <td>Matches: <td>123 </td></td>	Matches: <td>123 </td>	123
Percent Similarity:	100.00% <td>Conservative:</td> <td>0 </td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0 </td>	Mismatches:	0
Query Match:	24.49% <td>Indels:</td> <td>0 </td>	Indels:	0
DB:	27 <td>Gaps:</td> <td>0 </td>	Gaps:	0

US-09-935-124a-1 (1-1422) x US-60-197-873-15305 (1-123)

QY 102 ATGACCTCTTGGGGAGACCTGCGGAGCCGAGAGCGCTGCGCGCGGCTGCGGGAAA 161

DB 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProArgProAlaAlaGlyLyS 20

QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGATGACCTCCCGGACGAGATGACTCA 221

DB 21 GlnAlaGlnLySgLyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 40

QY 222 GAATCAGGGGACCTTTGCTTTTGAATCTCCACCGCTAGAGAGGAGATTCAGGT 281

DB 41 GlySerGlyLyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 60

QY 282 TCTCTGCAACATCAATATCCAGATGTTAAGACTGAAGGAGAAAGGACAAAGAAA 341

DB 61 SerLeuAlaThrSerLleSerGlnMetValYrThrGluGlyLySgLyValCySlySAla 80

QY 342 ACCTCCGAGAGAAAGAAATGGCAATGGCAAGCTTGTGAAAAGCC 401

DB 81 ThrSerGluGluGlnLySgLySerGluGlnLeuValGlnLySlySValCySlySAla 100

QY 402 TCTTGGGTATCTTTGCTCTGAGAGGCTATGTGGCTGAGCGGAGAGGTGAGAGGAGAG 461

DB 101 SerSerValIlePheGlyLeuYrGlyLyTyrValAlaGlnLySgLyGlnYrGluGlu 120

QY 462 ATGACGAT 470

DB 121 MetGlnAsp 123

RESULT 25

US-60-197-873-15305

Sequence 15305 Application US/60197873

GENERAL INFORMATION:

APPLICANT: Benjamin, Stephanie

APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Yves

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: 81 US1 PRO

CURRENT APPLICATION NUMBER: US/60/197,873

CURRENT FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 52153

SOFTWARE: Patent.pm

SEQ ID NO 15305

LENGTH: 123

TYPE: PRT

ORGANISM: Homo sapiens

US-60-197-873-15305

Alignment Scores:

Pred. No.:	2.56e-42	Length:	123
Score:	627.00 <td>Matches: <td>123 </td></td>	Matches: <td>123 </td>	123
Percent Similarity:	100.00% <td>Conservative:</td> <td>0 </td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0 </td>	Mismatches:	0
Query Match:	24.49% <td>Indels:</td> <td>0 </td>	Indels:	0
DB:	27 <td>Gaps:</td> <td>0 </td>	Gaps:	0

US-09-935-124a-1 (1-1422) x US-60-197-873-15305 (1-123)

QY 102 ATGACCTCTTGGGGAGACCTGCGGAGCCGAGAGCGCTGCGCGCGGCTGCGGGAAA 161

DB 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProArgProAlaAlaGlyLyS 20

QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGATGACCTCCCGGACGAGATGACTCA 221

DB 21 GlnAlaGlnLySgLyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 40

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Qy 222 GGATCAGGGGGA CCTTTGCTTTTGAATCTCCACCCGCTAGCAGTGGCATTCAGGT 281
    |||||||
Db 41 GlySerGlyGlyProLeuLeuPheAspAspLeuProAlaSerSerGlyAspSerGly 60
    |||||||
Qy 282 TCTCTTGCCACATCAATATCCAGATGTAAGACTGAAGGGAAAGAGCAAGAGAAA 341
    |||||||
Db 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGluGlyLysGlyAlaLysArgLys 80
    |||||||
Qy 342 ACCTCGAGAGAGAGAAATGGCAGTGAAGAGCTTGGAAGAAAGATTGTAAAGCC 401
    |||||||
Db 81 ThrSerGluGluGlnLysAsnGlySerGluGluLeuValGluLysLysValCysLysAla 100
    |||||||
Qy 402 TCTTCGTGATCTTTGCTCTGAAGGCTATGTGCTGAGCGAGGGGTGAGAGGAGAG 461
    |||||||
Db 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyGluArgGluGlu 120
    |||||||
Qy 462 ATGCAGGAT 470
    |||||||
Db 121 MetGlnAsp 123
    |||||||
```

Search completed: February 9, 2003, 18:10:37
Job time : 323.5 secs

OTHER INFORMATION: Serine/threonine phosphatases, family 2C,
OTHER INFORMATION: catalytic domain
US-10-072-012-853

Alignment Scores:
Pred. No.: 2,91e-20 Length: 260
Score: 422.50 Matches: 103
Percent Similarity: 56.18% Conservative: 56
Best Local Similarity: 36.40% Mismatches: 93
Query Match: 16.50% Indels: 31
DB: Gaps: 6

US-09-935-124a-1 (1-1422) x US-10-072-012-853 (1-260)

```
OY 417 GGTCTGAGAGGCTATGTGCTGAGCGAGAGGTGAGAGGAGAGATGACGATGCCAC 476
DB 9 GilyleuArgTyrGlyLysSerSerMetGlnGlyValArgLysPromeGluAspAlaHis 28
OY 477 GTGATCTGAGACATGACGAGAGGTGAGAGGCGCCCATGCTCTCATTAATCTCGAGTT 536
DB 29 ValIleThrProAspLeuSerGlyGlu-----AspSerGly 40
OY 537 TCATATTTGCTGCTTTTGAAGACATGAGAGAAATTCGACCTCAAAATTTGCTGACAG 596
DB 41 GlyPheHeGlyValPheAspGlyHisGlyGlySerGluAlaIleValPheLeuSerLys 60
OY 597 AATTGCAATCAAACTTAATCAAGAAATTTCTTAAAGATGATATACGTAGAGAA 656
DB 61 AsnLeuProGluIleLeuAlaGluGluLeuIleLysAspLys-----AspGluAspGlu 78
OY 657 ACCGTGAGAGATGCTTTTGGACACTTTGACACTATGATGAAGAGTTCTTAAACAA 716
DB 79 AspValGluAspAlaLeuArgLysAlaPheLeuArgThrAspGluIleLeuGluGlu 98
OY 717 GCTTCCAGCCAGAGCTGCTCGAAGATGGGTCACTGCCACGTGTGTTCTGGCTGA 776
DB 99 LeuGluSerLeuGluAspGln---ArgSerGlyThrThrAlaValAlaLeuIleArg 117
OY 777 GACAACTTTCTTATATTCGCAACTCGAGATGATGTCGGGCAATCTTGTCGTATAT 836
DB 118 GlyAsnLysLeuTyrValAlaAsnValGlyAspSerArgAlaValIleuCyseArgAsnGly 137
OY 837 GAGGAGAGTCMAAAACATGCAAGCTTAGCCTTCAGCAAGACATATCAACTCACTAT 896
DB 138 Lys-----AlaValGluLeuThrGluAspHisLeuProSerArgGlu 151
OY 897 GAAGAGCGATGAGATACAGAAAGCTGAGAGAAAGCTGAGGAGGGGCTTTGGAGC 956
DB 152 AspGluArgGluArgIleArgGluAlaGlyPheValSerAsnGlyArgValAsnGly 171
OY 957 GTGCTAGAGGTTCACGCTCCATTGGGACGGGCAATCAAGCGCTGGCGCTCACTCT 1016
DB 172 ValIleuAlaLeuSerArgAlaLeuGlyAsp---PheHeuLysProTyrValIleAla 190
OY 1017 GTGCCCAATCAAGACGCTCCAGCTGACCCCCAATGACAGTTCAATTTGTGGCTGT 1076
DB 191 GluProAspValThrValValGluLeuThrGluLysAspPheLeuIleuAlaSer 210
OY 1077 GATGGGCTCTTCAAGGCTTTTACCCGAGAGAGACCGTGAATCTTCTGCTCTC 1136
DB 211 AspGlyLeuTyrAspValIleuSerAsnGlnGlyValAlaAspIleVal----- 226
OY 1137 GAGGATGAAAAGATCCAGACCCGAGAGGAGATCCGACCGCCGCTACGAGACA 1196
DB 227 -----ArgLysHisLeuSerLysGlyLysProGlnGlu 237
OY 1197 GCCTGACAGAGCTGCGCAACAAGCGGTGACGCGGCTGCGGCGCAACAATCTCACTGTG 1256
DB 238 AlaAlaIalysLysLeuIleAspLeuAlaIleAlaArgGlySerLysAspAsnIleThrVal 257
OY 1257 ATGATGATG 1265
DB 258 ValValVal 260
```

RESULT 3

US-09-513-999C-7505

Sequence 7505, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glotard, J.Y.

TITLE OF INVENTION: Expresed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59, US2, REG

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent, pm

SEQ ID NO 7505

LENGTH: 86

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: UNSURE

LOCATION: 55

OTHER INFORMATION: Xaa=Phe or Leu

NAME/KEY: UNSURE

LOCATION: 56

OTHER INFORMATION: Xaa=Ala or Pro

NAME/KEY: UNSURE

LOCATION: 65

OTHER INFORMATION: Xaa=Glu or Lys

US-09-513-999C-7505

Alignment Scores:

Pred. No.: 1,59e-19 Length: 86
Score: 411.00 Matches: 83
Percent Similarity: 95.40% Conservative: 0
Best Local Similarity: 95.40% Mismatches: 3
Query Match: 16.05% Indels: 1
DB: Gaps: 0

US-09-935-124a-1 (1-1422) x US-09-513-999C-7505 (1-86)

```
OY 462 ATGCAAGATGCCCACTCATCTGAAACGACATCAAGAGAGTGAAGCCCATCTGCC 521
DB 1 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCyseArgProProSerSer 20
OY 522 CTCATTCTCGGGTTTCATATTTTGTGCTGTTTGTGATGACATGAGAGAAATTCGAGCTCA 581
DB 21 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyGlyIleArgAlaSer 40
OY 582 AAATTGCTGCACAGAAATTTGATCAAAACTTAATCAGAAATTTCTTAAAGAGATGTA 641
DB 41 LysPheAlaIleGlnAsnLeuHisGlnAsnLeuIleArgLys*****LysGlyAspVal 60
OY 642 ATCAGTGAAGAGAAACGCTGAAGAGATGCTTTTGGACACTTTCAGACATCTGATGAA 701
DB 61 IleSerValGlu***ThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGlu 80
OY 702 GAGTTCCTTAACAAGCTT 720
DB 81 Glu-SerLeuAsnLysLeu 86
```

RESULT 4
US-10-072-012-854
Sequence 854, Application US/10072012
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Paturajan, Meera
APPLICANT: Shimkets, Richard

```

/ APPLICANT: Li, Li
/ APPLICANT: Gangoli, Esba
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Futak, Katarzyna
/ APPLICANT: Grosse, William M.
/ APPLICANT: Alsbrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 854
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Protein
US-10-072-012-854

Alignment Scores:
Pred. No.: 5,3e-19 Length: 252
Score: 403.50 Matches: 104
Percent Similarity: 56.27% Conservative: 53
Best Local Similarity: 37.28% Mismatches: 85
Query Match: 15.76% Indels: 37
DB: 6 Gaps: 10

US-09-935-124A-1 (1-1422) x US-10-072-012-854 (1-252)
QY 433 CTGGCTGACCGAAGGTGAGAGGAGGAGATGCGCAGATCCTCATCTGAAGAC 491
DB 5 ValSerArgMetGlnIlyPheArgIlyPheMetGluAspAlaIleIleAlaGlyIlyAsn 24
QY 492 ATCACCGAGAGGTGTAGGCCCCCATCGCTCATTAATCGGTTTATTTGCTGT 551
DB 25 LeuAsnSerSerGlyIlyIlyAspSerIlyS-----GlyPhePheAlaVal 39
QY 552 TTGATGACATGAGGAATTGAGCCTCAAAATTGCTGCACAGAATTGATCAAAAC 611

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DB 40 PheArgGlyAsnGlyIlySerGlnAlaIleIlyIlyIleGlnIlyThrIlyS 59
QY 612 TTA---ATCAGAAA---TTTCTTAAGGAGATGTAATCAGTGTGAGAAAACSTGAAG 665
DB 60 LeuAlaLeuArgIlySerPheProGlnLeuAsp-----AspLeuGlnAsnAlaLeuIlyS 77
QY 666 AGATGCTTTTGGACATTTGACAGCATACTGATGAGAGTTCTTTAAACAGCTTCCAGC 725
DB 78 GluSerPheLeuGlnSer-----ThrAspGlnGlnLeu-----ArgSerSerAla 92
QY 726 CAGAAAGCTGCTGGAAGATGAGTCCAGTCCAGCTGTGTTCTGCTGTAGAACATTT 785
DB 93 AlaAsnThrAspLeuAspSerIlySerThrAlaValAlaLeuIleArgIlyAsnIlyS 112
QY 786 CTTTATATTTGCCAAGCTGAGAGATGTCGGCATCTTGCTGTTATATGAGAGAGT 845
DB 113 LeuIlyValAlaAsnValAlaGlyAspSerArgAlaValIleuCyAsnIly----- 127
QY 846 CAAAAACATGCAAGCTTAAGCTTCAGCAAGACATTAATCCAACTCAGTATGAGAGCGG 905
DB 128 AsnGlyAsnAlaIleIlyGlnLeuThrGlnAspHisIlyProSerAsnGlnAspGlnArg 147
QY 906 ATGAGATTCAGAAAGCTGAGGAAACGTC--AGGATGGGCGTGTGGGCGCTGCTA 962
DB 148 ArgArgIleGlnGlyAlaGlyIlyPheValSerArgAsnGlyArgValAsnGlyValIleu 167
QY 963 GAGTGTCAAGCTCCATTGGGGAGCGGACGATCAAG-----CGTGGCGGTTCACC 1013
DB 168 AlaValSerArgAlaPheGlnIlyAspPheGlnLeuIlySerProGlyValLeuGlnProValThr 187
QY 1014 TCTGTGCCGACATCAGACGCTGCAGCTGACCCCAATGACAGGTTGTTGTGGCC 1073
DB 188 AlaGlnProAspValThrSerHisIlySerIleThrProSerArgGlnPheLeuIleLeuAla 207
QY 1074 TGTGTGGCTCTTCAAGCTTTACCCCAAGAAAGCCGTGAATTCATCTTGCTGCT 1133
DB 208 SerAspGlyLeuIlyTrpAspValLeuSerAspGlnGlnValAlaSerIlyValArgSerGln 227
QY 1134 CTGAGAGTAAAGAAATGATCAGACCGGAGAGGAAGTCGACGCGCGCTACGAA 1193
DB 228 LeuSerAspGlyProMetGln----- 234
QY 1194 GCAGCCTGCAACAGGCTGCCCAACAGGCGGTGACGGGCTGCGGACGACAGCTC 1250
DB 235 ---AlaAlaGlnIlyLeuValAspTyrAlaIleAlaIlySerGlnAspAsnIle 252

RESULT 5
US-10-171-404A-46
/ Sequence 46, Application US/10171404A
/ GENERAL INFORMATION:
/ APPLICANT: BASF PLANT SCIENCE GMBH
/ TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
/ FILE REFERENCE: 16313-0119
/ CURRENT APPLICATION NUMBER: US/10/171,404A
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/295,680
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 46
/ LENGTH: 434
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-171-404A-46

Alignment Scores:
Pred. No.: 1.14e-15 Length: 434
Score: 353.50 Matches: 125
Percent Similarity: 44.71% Conservative: 65
Best Local Similarity: 29.41% Mismatches: 148
Query Match: 13.81% Indels: 87
DB: 6 Gaps: 19

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US-09-935-124A-1 (1-1422) x US-10-171-404A-46 (1-434)
QY 105 GACCTCTTGGGGACCTGCGGAGCCGAGCCG--TGGCGGCGCCGCTGCCGGGAA 161
DB 45 AspleuMetValSerLeuProgluThrSerSerCysSerValSerGlySerHisGlySer 64
QY 162 GAAGCTCAGAAAAGACCCCTGCTCTTGTATGACCTCCCTCGGCGACAGTACTGACTCA 221
DB 65 GluSerArgLyValLeuHisSerArgLyLeuSerProAlaMetCysGlySer 84
QY 222 GGATCAGGGGACCTTGTCTTTGTATCTCCACCCGCTAGACGTGGCGAT----- 275
DB 85 AlaAlaAlaAspIleValValAsp-----IleSerAlaGlyAspGluIle 100
QY 276 TCGAGTTCTCTTGCCACATCATCTCCAGATGTA--AAGACTGAAGGAAAGAGCA 332
DB 101 AengLySerAspValThrSerGluLySerMetIleSerArgThrGlu----- 116
QY 333 AAGAGAAAACCTCGAGAGAAAGAAATGCGAGAAAGCTTTGGAAAAAGAAATT 392
DB 117 -----SerArgSerLeuPheGluPheLyS-- 124
QY 393 TGTAAAGCTCTTGGTATCTTGTCTGAAGGCTATGTGCTGACCGGAGGTGAG 452
DB 125 -----SerValProLeuTyGlyPheThrSerIleCys-----GlyArg 137
QY 453 AGGAGAGAGATCAGAGATGCCACGTATCTGACACATATCCAGAGAGTGAAGCCC 512
DB 138 ArgProGluMetGluAspAla-----ValSerThrIleProArgPheLeuGlnSer 154
QY 513 CCATCGTCCCTCATT-----ACTCGGCTTTCATATTTTGGT 548
DB 155 SerSerGlySerMetLeuAspGlyArgPheAspProGlnSerAlaAlaHisAspPheGly 174
QY 549 GTTTTGTATGACATGAGAGAAATTCGAGCTCAAAATTTGTGTCAGAAATTTGCAACA 608
DB 175 ValTyArgGlyHisGlyGlySerGlnValAlaAsnTyArgGluArgMetHisLeu 194
QY 609 AACCTTAATCAGAAAATTTCTTAA-----GGAGATGTAATCAGT 647
DB 195 AlaLeuAlaGluGluIleAlaLySerGluPheMetLeuCysAspGlyAspThr--Trp 213
QY 648 GTAGAGAAACCGTAGAGAGTGCCTTTTGAACATTCAGACATGAGTAAGAGATTC 707
DB 214 LeuGluLySerTrp---LyLyAlaLeuPheAsnSerPheLeuArgValAspSerGluIle 232
QY 708 CTTAAACAGCTTCCAGCCAGAGACCTGCTCGAAGAGGTGCATCTGCCAGTGTT 767
DB 233 GluSerValAlaProGluThrVal-----GlySerThrSerValValAla 247
QY 768 CTGGCTGTAGACAACATTTCTTATATGCGAACCTCGAGATAGTCGGGCAATTTGTGT 827
DB 248 ValValPheProSerHisIlePheValAlaAsnCyGlyAspSerArgAlaValLeuCys 267
QY 828 CGTTATATGAGAGAGTCAAAAACATGACGCTTAAGCCTTAAGCCTCAGCAAAAGCATATATCCA 887
DB 268 Arg-----GlyLyThrAlaLeuPheLeuSerValAspHisLyPir 281
QY 888 ACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGGAAAGCTC-----AGG 938
DB 282 AspArgGluAspGluAlaAlaArgLyGluAlaAlaGlyLyValValIleGlnTrpAsn 301
QY 939 GATGGGCTGTTTGGGCGCTGAGAGGTGTCACGCTCACTTGGGAGCGGACAGTAAG 998
DB 302 GlyAlaArgValPheGlyValLeuAlaMetSerArgSerIleGlyAsp---ArgTyLeu 320
QY 999 CGCGCGGTCTCACCTCTGCGCCGACATCAGACGCTGCGACGTAGACCCCAATGACAG 1058
DB 321 LysProSerIleIleProAspProGluValThrAlaValLyAspValLyGluAspAsp 340
QY 1059 TTCATTTTGTGGCTGTGATGGCTCTTCAAGTCTTAACTCCCAAGAAAGCCGTGAAC 1118
DB 341 CysLeuIleLeuAlaSerAspGlyValTrpAspValMetThrAspGluAlaCysGlu 360
QY 1119 TTCATC-----TTGTCC 1130
DB 361 MetAlaArgLyArgLyIleLeuLeuTrpHisLyLyAsnAlaValAlaGlyAspAlaSer 380
QY 1131 TGTCTCGAGATGAAAAGATCCAGACCCGGAAGGAAAGTCCGACGCGCCGCTTAC 1190
DB 381 LeuLeuAlaAspGluArg-----ArgLyGluGlyLyS-----AspProAlaAla 395
QY 1191 GAAGCAGCTTGCAACAGGCTGCGCAACAGCGGTGACCGGGGCTCGCCGACACAGTC 1250
DB 396 MetSerAlaAlaGluTyLeuTyLeuSerLyLeuAlaIleGlnArgLySerLyAspAsnIle 415
QY 1251 ACTGTATGTGTGTG 1265
DB 416 SerValValValVal 420

RESULT 6
US-10-342-224-78 Application US/10342224
; Sequence 78, Application US/10342224
; GENERAL INFORMATION:
; APPLICANT: Nathalie Verbruggen
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress
; FILE REFERENCE: CN-012US
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US/10/342,224
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: EP 98202634.6
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-342-224-78

Alignment Scores:
Pred. No.: 1,3e-14 Length: 380
Score: 337.50 Matches: 102
Percent Similarity: 45.30% Conservative: 62
Best Local Similarity: 28.18% Mismatches: 129
Query Match: 13.18% Indels: 69
DB: 6 Gaps: 12

US-09-935-124A-1 (1-1422) x US-10-342-224-78 (1-380)
QY 273 GATTCAGCTTCTCTTGCACATCATATCCAGATGTAAG----- 314
DB 19 AspAsnThrSerSerAlaThrGluIleAspThrLeuGluAsnAspAspThrArgGln 38
QY 315 ---ACTAAGGGAAGAGCAAGCAAAAGAAAACCTCGAGAGAAAGAAATGCGAGTGA 371
DB 39 IleSerLyGlyLySerProProArgHisLeuThrSerSerAlaThrArgLeuGlnLeuAla 58
QY 372 GAGCTTGTGAAAAGAAATTTGT-----AAAGCTCT 404
DB 59 AlaAsnAlaAspValAspValCysAsnLeuValMetLySerLeuAspAspLySerGlu 78
QY 405 TCGGTGATCTTGTGTGTAAGGCTATGTGCTGAGCGGAAGGCTGAGAGAGATG 464
DB 79 PheLeuProValTyArgSerGlySerCysAlaIu---GlnLyAlaLySerIlePheMet 97
QY 465 CAGATGCCACATCTCTTCAACAGATCACCGAGAGTGTAGAGGCCCATGTCTCCTC 524
DB 98 GluAspGluHisIleCysIleAspAspLeuValAsnHisLeuGlyAlaAlaIleGlnCys 117
QY 525 ATTACTGGGTTTCATATTTTGTCTTTTGTATGACATGAGAAATTCAGACTCAGAAA 584
DB 118 SerSerLeuGlyAlaPheTyGlyValPheAspLyHisGlyLyThrAspAlaAlaHis 137

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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patent version 3.2
SEQ ID NO: 79625
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-79625

Alignment Scores:
Pred. No.: 1,63e-14      Length: 354
Score: 336.00           Matches: 100
Percent Similarity: 49.00%      Conservative: 47
Best Local Similarity: 33.33%    Mismatches: 105
Query Match: 13.12%           Indels: 48
Gap: 5                     Gaps: 12

US-09-935-124a-1 (1-1422) x US-09-724-676-79625 (1-354)

QY 417 GGTCTGAAGGCTATGTGCTGAGCGGAGGAGGAGGAGATGACGATGCCAC 476
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 21 GYLeuArgTYrGlyLeuSerSerMetGlnGlyTPArgValGluMetGluAspAlaHis 40

QY 477 GTATCTGAAGCATATCCAGAGATGAGGCCCGCATGCTCCATTAATCTCGGTT 536
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu---GluSerTrp 53

QY 537 TCATATTTTCTGTTTGTATGACATGAGGAAATTCGAAATTTGCTGCACAG 596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 54 SerPhePheAlaValTYrAspGlyHisAlaGlySerGlnValAlaIleValTYrCyS 73

QY 597 AATTTCATCAAACTTAATCAGAAATTTCT--AAAGAGAT-----GTATCAGT 647
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLYSerAlaGlyAlaProSer 93

QY 648 GTAGAGAAAACCGTGAAGAGATGCCCTTTTGACACTTTCAAGCATATGTAAGATTC 707
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 ValGlu---AsnValIleAsnGlyIleArgThrGlyPheLeuGlnIleAspGlnHisMet 112

QY 708 CTTAAACAGCTTCCAGACCATGCTGAGAACTGAGGCTCCACCTGTGTT 767
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 ArgValMetSerGlnIleValLeuHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132

QY 768 CTGCGTGTAGACACATTTCTTATATTTGCCAACCTCGGAGATAGTGGGCAATCTGTGT 827
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 LeuIleSerProGlnHisThrTYrPheIleAsnCYGlyAspSerArgGlyLeuLeuCYs 152

QY 828 CATTATATGAGAGAGTCAAAACATGACACCTTAAGCTCAGCAAGAACATATATCCA 887
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 Arg-----AsnArgIleValHisPhePheThrGlnAspHisIleValPro 166

QY 888 ACTCAGATATAGAGCGGATGAGATACAGAAAGCTGAGGAAACGTCAAGGATGGCGCT 947
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 SerAsnProLeuGlnIleValArgIleGlnAsnAlaGlyIleSerValMetIleGlnArg 186

QY 948 GTTTTGGCGCTGTAAGGTGTCAAGCTCCATTTGGGAGCGGACAGTACAAAGCGCTGC-- 1004
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 ValAsnGlySerIleuAlaValSerArgAlaLeuGlnIleAspPheAspTYrIleS--CyVal 205

QY 1005 -----GGTGTACCC-----TCTGTCCCGGACATCAGA 1031
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 206 HisGlyIleGlyProThrGlnGlnIleuValSerProGlnIleValHisAspIleGlu 225

QY 1032 CGCTGCAGCTGACCCCAATGACAGGTTTCATTTTGTGAGCTGTGATGGCTCTTCAG 1091
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCysAspGlyIleTrpAsp 243

QY 1092 GTCTTTTACCCCAAGAGAACCGGTGAATCTTATCTTGGCTGTCTGAG-----GATGAA 1145
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 ValMetGlyAsnGlnIleuLeuCYsAspPheValArgSerArgLeuGlnIleValHisAspAsp 263

QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACGCGAGCGCGCTGAGAAAGCAGCTGCAGAC 1205

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DB 264 -----LeuGlnIleValCYsAsn 269
QY 1206 AGCGTGGCCCAAGACGGCTGACAGCGGAGCTGGCCGACAAAGCATCATGATGTGTG 1265
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 270 GluValValAspThrCYsLeuTYrIleValGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 9
US-09-724-676-79626
Sequence 79626, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patent version 3.2
SEQ ID NO: 79626
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-79626

Alignment Scores:
Pred. No.: 1,63e-14      Length: 354
Score: 336.00           Matches: 100
Percent Similarity: 49.00%      Conservative: 47
Best Local Similarity: 33.33%    Mismatches: 105
Query Match: 13.12%           Indels: 48
Gap: 5                     Gaps: 12

US-09-935-124a-1 (1-1422) x US-09-724-676-79626 (1-354)

QY 417 GGTCTGAAGGCTATGTGCTGAGCGGAGGAGGAGGAGATGACGATGCCAC 476
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 21 GYLeuArgTYrGlyLeuSerSerMetGlnGlyTPArgValGluMetGluAspAlaHis 40

QY 477 GTATCTGAAGCATATCCAGAGATGAGGCCCGCATGCTCCATTAATCTCGGTT 536
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu---GluSerTrp 53

QY 537 TCATATTTTCTGTTTGTATGACATGAGGAAATTCGAAATTTGCTGCACAG 596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 54 SerPhePheAlaValTYrAspGlyHisAlaGlySerGlnValAlaIleValTYrCyS 73

QY 597 AATTTCATCAAACTTAATCAGAAATTTCT--AAAGAGAT-----GTATCAGT 647
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLYSerAlaGlyAlaProSer 93

QY 648 GTAGAGAAAACCGTGAAGAGATGCCCTTTTGACACTTTCAAGCATATGTAAGATTC 707
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 ValGlu---AsnValIleAsnGlyIleArgThrGlyPheLeuGlnIleAspGlnHisMet 112

QY 708 CTTAAACAGCTTCCAGACCATGCTGAGAACTGAGGCTCCACCTGTGTT 767
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 ArgValMetSerGlnIleValLeuHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132

QY 768 CTGCGTGTAGACACATTTCTTATATTTGCCAACCTCGGAGATAGTGGGCAATCTGTGT 827
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 LeuIleSerProGlnHisThrTYrPheIleAsnCYsIleAspSerArgGlyLeuLeuCYs 152

QY 828 CATTATATGAGAGAGTCAAAACATGACACCTTAAGCTCAGCAAGAACATATATCCA 887
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 Arg-----AsnArgIleValHisPhePheThrGlnAspHisIleValPro 166

QY 888 ACTCAGATATAGAGCGGATGAGATACAGAAAGCTGAGGAAACGTCAAGGATGGCGCT 947
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 SerAsnProLeuGlnIleValArgIleGlnAsnAlaGlyIleSerValMetIleGlnArg 186

QY 948 GTTTTGGCGCTGTAAGGTGTCAAGCTCCATTTGGGAGCGGACAGTACAAAGCGCTGC-- 1004
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 ValAsnGlySerIleuAlaValSerArgAlaLeuGlnIleAspPheAspTYrIleS--CyVal 205

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QY 1005 -----GGTGTACC-----TCGTGCCCGACATCAGA 1031
DB 206 HLeGlyLySgLyProThrgLugInLeuValSerProGluProGluValHisAepIleGlu 225
QY 1032 CGGTGCAGCTGACCCCAATGACAGTTTCATTTGTGGCCCTGTGATGGGCTTTCAAG 1091
DB 226 ArgSerGlu-----GluAapApGlnPheIleIleLeuValCysAapGlyIleTrpAap 243
QY 1092 GTCTTACCCAGAGAGAGCCGTGACTTCATCTGTCTGTCTGAG-----GATGAA 1145
DB 244 ValMetGlyAasnGluGluLeuCyAapPheValArgSerArgLeuGluValThrAapAap 263
QY 1146 AAGATCCAGACCCGGAGAGGAAATCCGACGCCGCGCTACGAGAGCAGCTTCAAC 1205
DB 264 -----LeuGluLySgLyAasn 269
QY 1206 AGGCTGCCAACAAGCGGTGACGCGGGCTCGGCCGACAACTCACTGTGATGGTGG 1265
DB 270 GluValValAapThrCysLeuTyTrpGlySerArgAapAapMetSerValIleLeuIle 289

RESULT 10
US-09-724-676-79627
; Sequence 79627, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79627
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-79627

Alignment Scores:
Pred. No.: 1,63e-14 Length: 354
Score: 336.00 Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12% Indels: 48
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-724-676-79627 (1-354)
QY 417 GGTCTGAAGGGCTATGTGGCTGACCGAAGGTGAGAGGAGAGATGCAGATGCCAC 476
DB 21 GtyleuAArgTyrgIleuSerSerMetGlnGlyTrpArgValGluMetGluAapIleHis 40
QY 477 GTCATCTGTAAGACATCAACCGAGAGTGAAGCCCAATCGCTTCATTAATCGGGT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu---GluSerTrp 53
QY 537 TCATATTTTGGCTTTTGGATGACATGAGAGATTCGAGCCCTCAAAATTTGCTGCAG 596
DB 54 SerPhePheAlaValTyArgPoliHisAlaGlySerGlnValAlaTyTrpCysGlu 73
QY 597 AATTGTCATCAAACTTAATCAGAAAATTTCT--AAAGAGAT-----GTATCACT 647
DB 74 HisLeuLeuAapHisIleThrAenAenGlnAapPheTyGlySerAlaGlyAlaProSer 93
QY 648 GTAGAGAAAAACCTGAGAGATGCTTTTGACACTTTCAGACATCTGATGAAGGTT 707
DB 94 ValGlyL--AasnValYsAenGlyIleArgTrpGlyPheLeuGluIleAapGluHisMet 112
QY 708 CTTAAACAGCTTCAGAGAGAGCTGCGCTGGAAGATGGTCCATCCAGCTGTGTT 767
DB 113 ArgValMetSerGluTybYsHisGlyAlaAapArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTAGACAAATCTTTATATATGCGCAACTCGAGATAGTGGGCAATCTTGTT 827

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DB 133 LeuIleSerProGlnHisThrTyArgPheIleAenCySgLyAapSerArgGlyLeuLeuCyS 152
QY 828 CTTATTAATGAGAGAGTCAAAAACATGACAGCTTAAGCCTCAAGCAAGCATATATCA 887
DB 153 Arg-----AasnArgYsValHisPhePheThrGlnAapHisIleSgPro 166
QY 888 ACTCAGATGAGAGAGCGAGATGAGATACAGAGGCTGAGAGAACTGACAGGATGGCGT 947
DB 167 SerAapProLeuGlnTybGluTybGlnIleGlnAenAlaGlyIleSerValMetIleGlnArg 186
QY 948 GTTTTGGGCTCTAGAGTGTCAAGCTTCATTTGGGAGAGCGGCAATACAGGCTGCG-- 1004
DB 187 ValAenGlySerLeuAlaValSerArgAlaLeuGlyAapPheAapTyTrp---CySVal 205
QY 1005 -----GGTGTACC-----TCGTGCCCGACATCAGA 1031
DB 206 HLeGlyLySgLyProThrgLugInLeuValSerProGluProGluValHisAepIleGlu 225
QY 1032 CGGTGCAGCTGACCCCAATGACAGTTTCATTTGTGGCCCTGTGATGGGCTTTCAAG 1091
DB 226 ArgSerGlu-----GluAapApGlnPheIleIleLeuValCysAapGlyIleTrpAap 243
QY 1092 GTCTTACCCAGAGAGAGCCGTGACTTCATCTGTCTGTCTGAG-----GATGAA 1145
DB 244 ValMetGlyAasnGluGluLeuCyAapPheValArgSerArgLeuGluValThrAapAap 263
QY 1146 AAGATCCAGACCCGGAGAGGAAATCCGACGCCGCGCTACGAGAGCAGCTTCAAC 1205
DB 264 -----LeuGluLySgLyAasn 269
QY 1206 AGGCTGCCAACAAGCGGTGACGCGGGCTCGGCCGACAACTCACTGTGATGGTGG 1265
DB 270 GluValValAapThrCysLeuTyTrpGlySerArgAapAapMetSerValIleLeuIle 289

RESULT 11
US-09-724-676A-79624
; Sequence 79624, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79624
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-79624

Alignment Scores:
Pred. No.: 1,63e-14 Length: 354
Score: 336.00 Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12% Indels: 48
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-724-676A-79624 (1-354)
QY 417 GGTCTGAAGGGCTATGTGGCTGACCGAAGGTGAGAGGAGAGATGCAGATGCCAC 476
DB 21 GtyleuAArgTyrgIleuSerSerMetGlnGlyTrpArgValGluMetGluAapIleHis 40
QY 477 GTCATCTGTAAGACATCAACCGAGAGTGAAGCCCAATCGCTTCATTAATCGGGT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu---GluSerTrp 53
QY 537 TCATATTTTGGCTTTTGGATGACATGAGAGATTCGAGCCCTCAAAATTTGCTGCAG 596
DB 54 SerPhePheAlaValTyArgPoliHisAlaGlySerGlnValAlaTyTrpCysGlu 73

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QY 597 AATTGCATCAAACTTAATCAAAAATTTCCT---AAGAGAT-----GTATCACT 647
Db 74 H1sleuEunaph1s1ethrAsnAnGlnAphPheIysSerAlGlyAlaProSer 93
QY 648 GTAGAGAAAACCGTGAAAGATGCTTTTGGACATTTCAAGCATATCATGAAGATTC 707
Db 94 ValGlu---AsnValIysAsnGlyIleArgThrGlyPheLeuGluValAspGlnHisMet 112
QY 708 CTTAAACAAAGCTTCAGCAGAAAGCTGCGAAAGATGGGTCACTGCCAGCTGTGT 767
Db 113 ArgValMetSerGlnIlyserHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTAGACAACTCTTATATATGCGCAACCTCGAGATATGTGGGCAATCTGTGT 827
Db 133 LeuIleSerProGlnHisThrIlyrPheIleAsnGlyAspSerArgGlyLeuLeuCys 152
QY 828 CGTTATATATAGAGAGATCAAAAACATGCACCTTAAGCCTCAAGCAAAAGACATATATCA 887
Db 153 Arg-----AsnArgIySerValHisPhePheThrGlnAspHisIlyserPro 166
QY 888 ACTCAGATATGAGAGCGCATATGAGATACAGAAAGCTGAGAAAGCTCAGGAGATGGGCT 947
Db 167 SerAsnProLeuGlnIlyserGlnArgIleGlnAsnHisIlySerValMetIleGlnArg 186
QY 948 GTTTGGGCGCTGTAGAGTGTCACTGCTTCATTTGGGAGCGGAGATCAAGCGCTGC--- 1004
Db 187 ValAsnGlySerLeuHisValSerArgAlaLeuGlyAspPheAspIlyrIys---CysVal 205
QY 1005 -----GGTGTCAAC-----TCTGTCCCGACATGCAG 1031
Db 206 HisGlyIlyserGlyProThrGlnGlnLeuValSerProGlnProGlnValHisAspIleGln 225
QY 1032 CGCTGCGAGCTGACCCCAATGACAGGTTCAATTTGTGGCTGTGATGGGCTCTTCAG 1091
Db 226 ArgSerGlu-----GlnAspArgGlnPheIleIleLeuHisCysAspGlyIlyleTrpAsp 243
QY 1092 GTCTTTACCCCAAGAAAGACCGGTGAATCTTCATCTTGTCCGTCTCGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnIlyserGlnArgSerArgGlnGlnValHisAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACGCGACGCCCGCTACAGACGCTGCAGAC 1205
Db 264 -----GGTGTCAAC-----LeuGlnIlyserValCysAsn 269
QY 1206 AGGCTGCGCAACAGCGGTGACGCGGCTCCGCGACAGCATCTGATGTGTGTG 1265
Db 270 GluValValAspThrCysLeuIlyrIysGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 12
US-09-724-676A-79625
; Sequence 79625, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79625
; LENGTH: 354
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-724-676A-79625

Alignment Scores:
Pred. No.: 1,63e-14 Length: 354
Score: 316.00 Matches: 100
Percent Similarity: 48.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12% Indels: 48
DB: Gaps: 12

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US-09-935-124a-1 (1-1422) x US-09-724-676A-79625 (1-354)
QY 417 GGTCTGAAGGCTATGTCTGAGCGGAAGGTGAGGAGGAGATGCAGATGCCAC 476
Db 21 G1yleuArgIyGlyIlyserSerMetGlnGlyTrpArgValGlnMetGlnAspHis 40
QY 477 GTCATCTCCAGACCACTTCAACCGAGAGGTAGAGGCCCCCATCTGCTTCATTCGGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerIlyLeu---GluSerTrp 53
QY 537 TCATATTTCTGCTTTTGTATGATGACATGAGAAATTCAGCCTCAAAATTTCTGCACAG 596
Db 54 SerPhePheAlaValIyrrAspGlyHisAlaGlySerGlnValAlaIyrrCysCysGln 73
QY 597 AATTGCGTCMAAACTTAATCAAAAATTTCCT---AAGAGAT-----GTATCACT 647
Db 74 H1sleuEunaph1s1ethrAsnAnGlnAphPheIysSerAlGlyAlaProSer 93
QY 648 GTAGAGAAAACCGTGAAAGATGCTTTTGGACATTTCAAGCATATCATGAAGATTC 707
Db 94 ValGlu---AsnValIysAsnGlyIleArgThrGlyPheLeuGluValAspGlnHisMet 112
QY 708 CTTAAACAAAGCTTCAGCAGAAAGCTGCGAAAGATGGGTCACTGCCAGCTGTGT 767
Db 113 ArgValMetSerGlnIlyserHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTAGACAACTCTTATATATGCGCAACCTCGAGATATGTGGGCAATCTGTGT 827
Db 133 LeuIleSerProGlnHisThrIlyrPheIleAsnGlyAspSerArgGlyLeuLeuCys 152
QY 828 CGTTATATATAGAGAGATCAAAAACATGCACCTTAAGCCTCAAGCAAAAGACATATATCA 887
Db 153 Arg-----AsnArgIySerValHisPhePheThrGlnAspHisIlyserPro 166
QY 888 ACTCAGATATGAGAGCGCATATGAGATACAGAAAGCTGAGAAAGCTCAGGAGATGGGCT 947
Db 167 SerAsnProLeuGlnIlyserGlnArgIleGlnAsnHisIlySerValMetIleGlnArg 186
QY 948 GTTTGGGCGCTGTAGAGTGTCACTGCTTCATTTGGGAGCGGAGATCAAGCGCTGC--- 1004
Db 187 ValAsnGlySerLeuHisValSerArgAlaLeuGlyAspPheAspIlyrIys---CysVal 205
QY 1005 -----GGTGTCAAC-----TCTGTCCCGACATGCAG 1031
Db 206 HisGlyIlyserGlyProThrGlnGlnLeuValSerProGlnProGlnValHisAspIleGln 225
QY 1032 CGCTGCGAGCTGACCCCAATGACAGGTTCAATTTGTGGCTGTGATGGGCTCTTCAG 1091
Db 226 ArgSerGlu-----GlnAspArgGlnPheIleIleLeuHisCysAspGlyIlyleTrpAsp 243
QY 1092 GTCTTTACCCCAAGAAAGACCGGTGAATCTTCATCTTGTCCGTCTCGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnIlyserGlnArgSerArgGlnGlnValHisAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACGCGACGCCCGCTACAGACGCTGCAGAC 1205
Db 264 -----GGTGTCAAC-----LeuGlnIlyserValCysAsn 269
QY 1206 AGGCTGCGCAACAGCGGTGACGCGGCTCCGCGACAGCATCTGATGTGTGTG 1265
Db 270 GluValValAspThrCysLeuIlyrIysGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 13
US-09-724-676A-79626
; Sequence 79626, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222

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[illegible][illegible]


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Db 206 HieglylyglyProthrgluInleuValserProgluValHisaprlleglu 225
Qy 1032 CGGTGGACACTACACCCCAATGACAGCTTATTTGGCTGTGATGGCTCTCAAG 1091
Db 226 Ariserglu-----GluasppspglnPhilelleleuAlaCyAspBglyIletrpAsp 243
Qy 1092 GTCTTATCCCGAAGAAAGCCGTGAATCTTCTGTCTGTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGluInleuCyAspPheValArgSerArgleuGluValThrAspAsp 263
Qy 1146 AGATTCAGACCCGGGAAAGGAGAGTCCGACGCCGCTACGAAAGACCTTCAGC 1205
Db 264 -----LeuGluIlyValCysAsn 269
Qy 1206 AGCTGGCCACAGACGCGGTGACGCGGCTCGCCGACACGTCATGTGATGTGTG 1265
Db 270 GluValValAspThrCysLeuTyrlglySerArgAspAsnMetSerValIleleuIle 289

RESULT 15
US-10-168-506-21
; Sequence 21, Application US/10168506
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDASANAM, SUCHA
; APPLICANT: RILU, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168, 506
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-506-21

Alignment Scores:
Pred. No.: 4,086-14 Length: 360
Score: 330.00 Matches: 99
Percent Similarity: 47.63% Conservative: 62
Best Local Similarity: 29.28% Mismatches: 117
Query Match: 12.89% Indels: 60
DB: Gaps: 13

US-09-935-124A-1 (1-1422) x US-10-168-506-21 (1-360)
Qy 303 CAGATGTAAGACTGAAGGAAAGGACAAAGAAACCTCCGAGAGAGAAAGAT 362
Db 57 LysMetValIySerIyS-----ValAlaGluThrMetGlnAsnAspArgleu 72
Qy 363 GGCAGTGAAGAGCTTGTGAAAGAAAGTTGTAAAGCTCTTCGTGATCTTGGTGTG 422
Db 73 GlyGlyLeuAspValleuGluAlaGluPheSerIySThr-----TyrIuPhe 88
Qy 423 AAGGCTAT-----GTGCTGAGCGAGAGGCTGAGAGGAGAGATGAGAGATGCC 473
Db 89 LysAsnHisAsnValAlaValIySerIleGlnGlyArgArgAspHisMetGluAspArg 108
Qy 474 CAGCTCATCTGAACGACATCACCGAGAGGTAGAGCTGAGCCCTCATCTCTCTGCG 533
Db 109 PheGluValIleuThrAspLeuAlaAsnIySThrHisPro-----TyrIuPhe 121
Qy 534 GTTCAATATTTTGTGCTTTTGTGATGAGATGAGAGATGAGAGATGAGAGATTTGTGCA 593
Db 122 ---SetIlePheGlyIlePheAspGlyHisGlyGluThrAlaAlaGluTyrValIys 140

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Qy 594 CAGAAATTTG-----CATCAAACTTAATGCAAAATTTCTTAAGGA 635
Db 141 SerArgLeuProgluAlaLeuIySglnHisSteGlnAspTyrGluIyAspIySglnAsn 160
Qy 636 GATGTAATCATGATGAGAAACCGTGAAAGAGATGCTTTTGGACACTTTCAGACACT 695
Db 161 SerValleuSerTyrGlnThrIleleuGluGlnGlnIleleuSer-----Ile 176
Qy 696 GATGAAGAGTCTTAAACAGCTTCAGCCAGCAAGACCTGCTGAAAGATGGGTCCACT 755
Db 177 AspArgGluMetLeuGluIyLeuThrValSer-----TyrAspGluAlaGly 192
Qy 756 GCCAGGTGCTCTGCTGTA-----GACAACTTTTATATGCAACTCGAGAT 809
Db 193 ThrThrCysleuIleAlaIleuLeuSerAspIyAspLeuThrValAlaAsnValGlyAsp 212
Qy 810 AGTCGGCAATCTTGTCTGTATTAAGAGAGAGTCAAAACATGACGCTTAAAGCTTC 869
Db 213 SerArgGlyValIleuCys-----AspIyAspGlyAsnAlaIleProleu 227
Qy 870 AGCAAAAGCATATTCCACTGATTAAGAGCCGATGAGATTCAGAGGCTCGAGCA 929
Db 228 SerHisAspHisIyAspTyrGlnleuIySglnArgIyLeuIyAspAlaGlyGly 247
Qy 930 AACGTCAG-----GATGCGCTGTTTGGGCTGTAGAGTGTACGCTCCATT 980
Db 248 PheIleSerPheAsnGlySerTyrArgValGlnGlyIleleuAlaMetSerArgSerIle 267
Qy 981 GGGAGCGGAGATACAGAGCGCTGCGGTGCACC---TCTGTCCCGACATCAGACGCTGC 1037
Db 268 GlyAspTyrProleuIyAsnIleuAsnValIleProAspPheAspIleleuThrPhe 287
Qy 1038 CAGCTGACCCCC---AATGACAGTTCATTTTGTGAGCTGTGATGAGGCTTCAAGTTC 1094
Db 288 AspLeuAspIySleuGlnProgluPheMetIleleuAlaSerAspGlyLeuTyrAspAla 307
Qy 1095 TTTAACCCCAAGAAAGCCGTGAACCTGATCTGTGCTGTGAGAGATGAAGAAATCAG 1154
Db 308 PheSerAsnGluGluAlaValArgPheIleIySglnArgleuAspGluProHisPheGly 327
Qy 1155 ACCCGGAAAGGAAATCCCGACGCGACGCGCCGCTACGAAAGACCTTCGACAGGCTGCC 1214
Db 328 AlaIySer-----IleVal 332

Qy 1215 AACAAAGCGGTGACAGCGGCTCGGCCGACACGTCATCTGTGATGTGTGCGG 1268
Db 333 LeuGlnSerPheTyrArgGlyCysProAspAsnIleThrValMetValIyS 350

RESULT 16
US-10-311-764-1
; Sequence 1, Application US/10311764
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
; APPLICANT: BAUGHN, Mariah R.; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.
; APPLICANT: GRIFFIN, Jennifer A.; HAPALA, April J.A.
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
; APPLICANT: LU, Yan; NGUYEN, Daniel B.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: KENDY, Roopa M.; SANKARANARAYAN, Madhusudan M.
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.
; APPLICANT: CHAMLA, Narinder K.; YANG, Junming
; APPLICANT: YAO, Monique G.; YUE, Henry
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0126 USN
; CURRENT APPLICATION NUMBER: US/10/311,764
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19442
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/212,447
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/213,746

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/ PRIOR FILING DATE: 2000-06-22
/ PRIOR APPLICATION NUMBER: US 60/215,210
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 60/216,529
/ PRIOR FILING DATE: 2000-07-06
/ PRIOR APPLICATION NUMBER: US 60/218,080
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/220,117
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PERL Program
/ SEQ ID NO 1
/ LENGTH: 372
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Inctye ID No: 8124196CD1
US-10-311-764-1

Alignment Scores:
Pred. No.: 2,98e-13 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.32% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
DB: 6 Gaps: 15

US-09-935-124a-1 (1-1422) x US-10-311-764-1 (1-372)
QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGAGTACTGATCA----- 221
DB 27 LeuLeuGlnAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
QY 222 -----GGATCAGGGGACCTTTGCTTTTATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTyrAspAsnProGlyIle 66
QY 252 -----CTCCACCCGCTAGCAGTGCGCATTCAGGT 281
DB 67 TyrAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTTCCACATCAATATCCAGATGTTAAGACTGAAGGAGAAAGAGAGAGAAAA 341
DB 81 ----- 81
QY 342 ACCTCCGAGAGAGAGAAATGGCACTGTGTGAAAAAGAAAGTTGTAAAGCC 401
DB 82 -----LysTyrGly-----LysProIleProIle 90
QY 402 TCTTCGGTATCTTTGATCTGAAGGCTATGTGCTGAGCGGAAAGGATGAGAGAGAG 461
DB 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgLys--GluAsnGluAsp 109
QY 462 ATGCAGAGATGCCACGTCATCTGAAAGACATCACCGAGAGGTAGAGCCCATGCTCC 521
DB 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
QY 522 CTCATTAACCTCGGTTTCATATTTTGTCTTTTGTATGAGACATGAGAGAAATTCAGCCTCA 581
DB 120 -----ValLeuTyrPheAlaValTyrAspGlyHisGlyGlyProAlaAlaAla 135
QY 582 AATTTGTCGACAGATTGTCATCAAACTTAATCAGAAATTTCTTAAAGAGATGTA 641
DB 136 AspPheCysHisThrHisMetGluLysCysIleMetAspLeuLeuProLys----- 152
QY 642 ATCAGTGTAGAGAAAAACGTTAGAGATGCTTTTGACACTTTCAAGCATACGTAGTAA 701
DB 153 -----GluLysAsnLeuGluTyrThrLeuLeuThrLeuAlaPheLeuGluIleAspLys 169
QY 702 GAGTTCCTTAAACAGCT-----TCCAGCCAGAGAGCTGCCCTGGAAGATGGTGCACCT 755
DB 170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
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QY 756 GCCAGTGTGTTCTGCTGTAGACAACATT---CTTTATATGCCAACCTCGAGATAGT 812
DB 190 AlaThrValAlaLeuLeuAspArgGlyIleGluLeuValValAlaSerValGlyAspSer 209
QY 813 CGGGCAATTTGTGTGCTTATATAGAGAGACTCAAAAACATGACGCTTAAAGCTCAGC 872
DB 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetCysLeuThr 223
QY 873 AAAGGACATTAATCCAACTCAGTATGAGAGCGGATGAGATACAGAGCTCGAGAGA--- 929
DB 224 IleAspHisThrProGluArgLysAspGluLysGluArgIleLysLysCysGlyLysPhe 243
QY 930 -----ACGTCAGGATGGGCGCTTTTGCGGCTGTAGAGGTCTCAAGCTCC 977
DB 244 ValAlaTyrAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
QY 978 ATTGGGAGCGGCGAGTACAAAGCGCTGCGGTCTACCTCTGTGCGCCGACATCAGAGCTGC 1037
DB 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTTCACTTTGTGGGCTGTGATGGGCTCTCAAGTTC 1094
DB 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTTACCCCAAGAAAGACCGCGTCACTTCACTTGTCTGTCTGTGAGAGATGAAAGATCCAG 1154
DB 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
QY 1155 ACCCGGAAAGGAGAGTCCGACCGACCGCCGCTAGAAAGCAGCTGCACAGGCTGCGCC 1214
DB 322 -----AlaAlaHisIleAlaValThr 327
QY 1215 AACAGCGGCTGTCAGCGGGCTCGGCGGACACGTCATGTATGATGGTGGCGATTAGGC 1274
DB 328 GluGlnAlaIleGlnTyrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
QY 1275 CACTGAGGGGTGCGCGCGCCGACGAG 1301
DB 348 AlaTyrGlyLysTyrLysAsnSerGlu 356

RESULT 17
US-09-724-676-80004
/ Sequence 80004, Application US/09724676
/ GENERAL INFORMATION:
/ APPLICANT: Compugen LTD
/ TITLE OF INVENTION: Variants of alternative splicing
/ FILE REFERENCE: 128181.4 Compugen
/ CURRENT APPLICATION NUMBER: US/09/724,676
/ CURRENT FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 97222
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 80004
/ LENGTH: 327
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-724-676-80004

Alignment Scores:
Pred. No.: 5.46e-13 Length: 327
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: 5 Gaps: 8

US-09-935-124a-1 (1-1422) x US-09-724-676-80004 (1-327)
QY 333 AAGAGAAAAACCTCGAGAGAGAGAAAGATGCGAGCTGTGGAAAAAGAAAGTT 392
DB 7 LysProLysThrGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
QY 393 TGTAAGCTCTTCGGTATCTTTGCTGTAAGGCTATGTGCTGAGCGGAAGGATGAG 452
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Oy 1125 TTGTCCTGTCGAGAGTAAAGATCCAGACCCGGAGGAAAGTCCGACCCGACGCC 1184
    |||
Db 259 LysSerArgLeuLl-----ValSerAsp 266
Oy 1185 CGCTACGAAGACCGCTGCAACAGCGTCGCCAACAGCGCGTCGAGGGGCTCGGCCGAC 1244
    |||
Db 267 AspleuGluAsnValCyAsnThrValValAspThrCysLeuHisIleuSglYserHArgAsp 286
Oy 1245 AACGTCACTGTGATGGTGTG 1265
    |||
Db 287 AsnMetSerIleValLeuVal 293

RESULT 19
US-09-724-676-80002
; Sequence 80002, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80002
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80002

Alignment Scores:
Pred. No.: 5.5e-13 Length: 387
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-09-724-676-80002 (1-387)
Oy 333 AAGAGAAAACCTCGAGAGAGAAAGATGCGACGTGAGAAAGCTTGTGAAAAGAAATT 392
    |||
Db 7 LysProlYstHnGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
Oy 393 TGTAAAGCCTTCGCGTATCTTGGCTGTAAGGGCTATGCGCTGAGCGGAAGGTGAG 452
    |||
Db 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTrp 32
Oy 453 AGGAGAGATGACAGATGCCACGTCATCTGAAACGACATCAACGAGAGGTGAGGCC 512
    |||
Db 33 ArgValGluMetGluAspAlaHisThrAlaValAlaGlyIle----- 46
Oy 513 CCATGTCCTCCATTAAGTGGGTTTCATATTTGCTGTTTGGATGAGAGAAATT 572
    |||
Db 47 ProHisGlyLeu--GluAspTrpSerPheAsnAlaValTyrAspGlyHisIleGlySer 65
Oy 573 CGAGCCTCAAAATTTGCTGACAGAAATTTGCATCAAAATTAATCAGA----- 620
    |||
Db 66 ArgValAlaAsnTyrCysSerThrHisLeuLeuGluHisIleThrThrAsnGluAspPhe 85
Oy 621 -----AAATTTCTAAAGAGATGTATCATGTTAGAGAAAACGTTGAAGAGA 668
    |||
Db 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGluLeuSerValGlu--AsnValLysAsn 104
Oy 669 TGCCTTTTGGACATTTCAAGCATCTGATGAAAGATTCTTAAACACATTTCCAGCCAG 728
    |||
Db 105 GlyIleLeuGlnGlyPheLeuLysIleAspGluTyrMetArgAsnPheSerAspLeuAsp 124
Oy 729 AAGCTGCTGGAAGATGGTGCACCTGCTGACAGCGTGTGCTGCTGTATAGCAACATTTCT 788
    |||
Db 125 AsnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetIleSerTrpLysHisIle 144
Oy 789 TATATTTGCCAACCTCGAGATAGTCGGGCAATCTTGTGCTTATATATGAGAGATCAA 848
    |||
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Db 145 TyrPheIleAsnCysGlyAspSerArgAlaValLeuTyrArgAsnGlyGln----- 161
Oy 849 AAACATGACAGCTTAAAGCCTGACGAAAGACATATCCAACTGATATGAAAGCGCATG 908
    |||
Db 162 -----ValCysPheSerThrGlnAspHisLysProCysAsnProArgGluLysGln 178
Oy 909 AGGATACAGAAAGCTGAGAGAAACCTGACAGGATGGCGCTGTTTGGCGCTGTAGAGGTG 968
    |||
Db 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
Oy 969 TCACGCTCCATTTGGGAGCGGACGACATCAAGCGCTCCGCT----- 1007
    |||
Db 199 SerArgAlaLeuGlnLysAspTyrAspTyrLysCysValAspGlyLysGlyProThrGluGln 218
Oy 1008 ---GTCACCTGTCGTCGCCGACATCAGACGCTGCCAGTCGACCCCAATGACAGTTCAAT 1064
    |||
Db 219 LeuValSerProGluProGluValTyrGluIleLeuAlaGluGluAspGluPheIle 238
Oy 1065 TTGTTGGCCTGTGATGGCTCTTCAAGGCTTTTACCCGAGAGAAAGCGGTGAATTTCATC 1124
    |||
Db 229 IleLeuAlaCysAspGlyIleTyrAspValMetSerAsnGluGluLeuCysGluTyrVal 258
Oy 1125 TTGTCCTGTCGAGAGTAAAGATCCAGACCCGGAGGAGAACTCCGACCCGACGCC 1184
    |||
Db 259 LysSerArgLeuGlu-----ValSerAsp 266
Oy 1185 CGCTACGAAGACCGCTGCAACAGCGTCGCCAACAGCGCGTGCAGCGGCTCGGCCGAC 1244
    |||
Db 267 AspleuGluAsnValCyAsnThrValValAspThrCysLeuHisLysGlySerArgAsp 286
Oy 1245 AACGTCACTGTGATGGTGTG 1265
    |||
Db 287 AsnMetSerIleValLeuVal 293

RESULT 20
US-09-724-676-80003
; Sequence 80003, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80003
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80003

Alignment Scores:
Pred. No.: 5.5e-13 Length: 387
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-09-724-676-80003 (1-387)
Oy 333 AAGAGAAAACCTCGAGAGAGAAAGATGCGACGTGAGAAAGCTTGTGAAAAGAAATT 392
    |||
Db 7 LysProlYstHnGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
Oy 393 TGTAAAGCCTTCGCGTATCTTGGCTGTAAGGGCTATGCGCTGAGCGGAAGGTGAG 452
    |||
Db 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTrp 32
Oy 453 AGGAGAGATGACAGATGCCACGTCATCTGAAACGACATCAACGAGAGGTGAGGCC 512
    |||
Db 33 ArgValGluMetGluAspAlaHisThrAlaValAlaGlyIle----- 46
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QY 513 CCATGTCCTCATTAATCGGGTTTCATATTTTCTGTTTGTGACATGAGAAATT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 ProHlsglyLeu---gluAspTTPserPhehlaValIyzaBpGlyhlaBalglySer 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 CGAGCCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTAATCAGA----- 620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 ArgValAlaAsnTYrCyseSerThrhIleuLeuGlnhIleThrhAsnGluAspPhe 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 621 -----AAATTTCTTAAGAGATGTAACTGATGTAGAGAAACCGTGAAGAGA 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ArgAlaAlaGlyLyseSerGlySerAlaLeuGlnIleuSerValGlu---AsnValLyseAsn 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 669 TGCCTTTTGACACTTTCAAGCATATGATGAAGAGTTCTTTAAACAGCTTCCAGCCAG 728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 GlyIleArgThrhGlyPheLeuLyIleAspGlyTyMetArgAsnPhseSerAspLeuArg 124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 729 AAGCCTCGCTGGAAGATGGTGCACCTGCGCAGCTGTGTTCTGCTGATGAACAATTCTT 788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 AsnGlyMetAspArgSerGlySerThrhAlaValGlyValMetIleSerProLyshIle 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 789 TATATTGCCAAGCTGAGATAGTCGGGCAATCTGTGTCGTTAATGAGAGAGTCAA 848
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 TyrPheIleAsnCyseGlyAspSerThrhAlaValLeuTyArgAsnGlyGln----- 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 849 AAACATGCAGCCTTAAGCTCAGCAAGAAAGACATTAATCCAACTCAATGAGAGCGGATG 908
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 -----ValCysePheSerThrhAlaAspIleLyseProCyAsnProArgGlyLyseGlu 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 909 AGGATTCAGAAAGGCTTGAGAGAAACGTCAAGGATGGCGCTGTTTGGCGCTTCAAGCTG 968
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 ArgIleGlnAsnAlaGlyGlyIySerValMetIleGlnArgValAsnGlySerIleuAlaVal 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 969 TCACGCTCCATTGGGGAGCGGAGATACAGACGCTGCGGT----- 1007
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 SerArgAlaLeuGlyAspTyArgPtyrIlyCyseValAspGlyLyseGlyProThrhGluGln 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1008 ---GTCACCTCTGTGCCGACATCAGACGCTGCCAGCTGACCCCAATGACAGGTTCAAT 1064
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 LeuValSerProGluProGluValTyArgIlyIleuArgAlaGlyGluAspGluPheIle 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1065 TTGTTGGCTGTGATGGGCTTTCAAGGCTTTTACCCCAAGAAAGACCGGTGAACCTTCATC 1124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 IleuValIleAsnGlyIlyIleThrpAspValMetSerAsnGlyGlyIleuCyseGlyTyVal 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1125 TTGTCCTGTCTGAGATGAAGAAATCCAGACCCGGGAAGGAGATCCGACGCCGACGCC 1184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 LysSerArgLeuGln-----ValSerAsp 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1185 CGCTACGAGACGCTTCGACAGCTGGCCAAAGAGCGGTGACAGCGGCGCTCGCGCGAC 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AspLeuGluAsnValCyseAsnTrpValValAspThrCyseuThIlyseGlySerArgAsp 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1245 AACGTCACTGTGATGTGTG 1265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 AsnMetSerIleValLeuVal 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 21
US-09-724-676A-80002
; Sequence 80002, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80002
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-80002

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Alignment Scores:
Pred. No.: 5,se-13 Length: 387
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatch: 125
Query Match: 12.23% Indel: 56
DB: Gaps: 8

US-09-935-124a-1 (1-1422) x US-09-724-676A-80002 (1-387)
QY 333 AAGAGAAACCTCCGAGAGAAAGAAAGATGGCAGTGAAGAGCTTGAGAAAGAAATT 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 LysProLyseThrhGlyLyshIleAsnAlaIleGlyAlaGlyAsn----- 20
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 393 TGTAAAGCTTTCGGTGATCTTTGCTTGAAGGCTATGTGGCTGACCGGAGGGTGAAG 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 -----GlyLeuAspGlyTyArgIlyLeuSerSerMetGlnGlyTyArg 32
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 453 AGGAGAGATGACAGATGCCACGTCAATCCGAAAGATCCAGACCGAGAGTGAAGCCC 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 ArgValGluMetGluAspAlaIleThrhAlaValAlaGlyIle----- 46
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 CCATGTCCTCATTAATCGGGTTTCATATTTTCTGTTTGTGACATGAGAAATT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 ProHlsglyLeu---gluAspTTPserPhehlaValIyzaBpGlyhlaBalglySer 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 CGAGCCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTAATCAGA----- 620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 ArgValAlaAsnTYrCyseSerThrhIleuLeuGlnhIleThrhAsnGluAspPhe 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 621 -----AAATTTCTTAAGAGATGTAACTGATGTAGAGAAACCGTGAAGAGA 668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ArgAlaAlaGlyLyseSerGlySerAlaLeuGlnIleuSerValGlu---AsnValLyseAsn 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 669 TGCCTTTTGACACTTTCAAGCATATGATGAAGAGTTCTTTAAACAGCTTCCAGCCAG 728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 GlyIleArgThrhGlyPheLeuLyIleAspGlyTyMetArgAsnPhseSerAspLeuArg 124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 729 AAGCCTCGCTGGAAGATGGTGCACCTGCGCAGCTGTGTTCTGCTGATGAACAATTCTT 788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 AsnGlyMetAspArgSerGlySerThrhAlaValGlyValMetIleSerProLyshIle 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 789 TATATTGCCAAGCTGAGATAGTCGGGCAATCTGTGTCGTTAATGAGAGAGTCAA 848
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 TyrPheIleAsnCyseGlyAspSerThrhAlaValLeuTyArgAsnGlyGln----- 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 849 AAACATGCAGCCTTAAGCTCAGCAAGAAAGACATTAATCCAACTCAATGAGAGCGGATG 908
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 -----ValCysePheSerThrhAlaAspIleLyseProCyAsnProArgGlyLyseGlu 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 909 AGGATTCAGAAAGGCTTGAGAGAAACGTCAAGGATGGCGCTGTTTGGCGCTTCAAGCTG 968
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 ArgIleGlnAsnAlaGlyGlyIySerValMetIleGlnArgValAsnGlySerIleuAlaVal 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 969 TCACGCTCCATTGGGGAGCGGAGATACAGACGCTGCGGT----- 1007
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 SerArgAlaLeuGlyAspTyArgPtyrIlyCyseValAspGlyLyseGlyProThrhGluGln 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1008 ---GTCACCTCTGTGCCGACATCAGACGCTGCCAGCTGACCCCAATGACAGGTTCAAT 1064
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 LeuValSerProGluProGluValTyArgIlyIleuArgAlaGlyGluAspGluPheIle 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1065 TTGTTGGCTGTGATGGGCTTTCAAGGCTTTTACCCCAAGAAAGACCGGTGAACCTTCATC 1124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 IleuValIleAsnGlyIlyIleThrpAspValMetSerAsnGlyGlyIleuCyseGlyTyVal 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1125 TTGTCCTGTCTGAGATGAAGAAATCCAGACCCGGGAAGGAGATCCGACGCCGACGCC 1184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 LysSerArgLeuGln-----ValSerAsp 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1185 CGCTACGAGACGCTTCGACAGCTGGCCAAAGAGCGGTGACAGCGGCGCTCGCGCGAC 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AspLeuGluAsnValCyseAsnTrpValValAspThrCyseuThIlyseGlySerArgAsp 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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OY 1245 AACGCTACGTGATGCTGATG 1265
Db 287 AemMetSerIleValLeuVal 293

RESULT 22
US-09-724-676A-80003
/ Sequence 80003, Application US/09724676A
/ GENERAL INFORMATION:
/ APPLICANT: Comugen LTD
/ TITLE OF INVENTION: Variants of alternative splicing
/ FILE REFERENCE: 129181.4 Comugen
/ CURRENT APPLICATION NUMBER: US/09/724,676A
/ CURRENT FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 97222
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 80003
/ LENGTH: 387
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-724-676A-80003

Alignment Scores:
Pred. NO.: 5.5e-13 Length: 387
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-09-724-676A-80003 (1-387)
OY 333 AAGAGAAAAACCTCCGAGAGAGAGAAAGATGACATGAGAGCTTGTGGAAAAAGAAATT 392
Db 7 LyseProLySerThrGluValHisAspAlaMetIleValAlaGluValen----- 20
OY 393 TGTAAAGCTCTCCGCTGATCTTTTGGTGTGAAGGCTATGTGCTGAGTGCAGGAGGTGAG 452
Db 21 -----GlyLeuAlaGlyArgGlyLeuSerSerMetGlnGlyTyr 32
OY 453 AGGAGGAGATGACGAGATGCCAGCATCTCTGTAAACAGATCAACCGAGAGGTGTAGGCC 512
Db 33 ArgValAlaGluMetGluAspAlaHisThrAlaValAlaGlyLe----- 46
OY 513 CCATGCTCCCTCATTTACTCCGGGTTTTCATATTTCTGTGTTTGTATGAGACATGAGGATT 572
Db 47 ProHisGluLeu---GluAspTyrSerPhePheHisAlaValTyrAspGlyHisAlaGlySer 65
OY 573 CGAGCCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTAATCAGA----- 620
Db 66 ArgValAlaAsnTyrCysSerThrHisLeuLeuMetIleHisThrHisAsnGluAspPhe 85
OY 621 -----AATTTCCTAAAGAGATGTATATCACTGATGAGAGAAACCGTGAAGAGA 668
Db 86 ArgAlaAlaGlyLeuSerGlySerAlaLeuGluLeuSerValGlu---AsnValLyAsn 104
OY 669 TGCCTTTTGACACTTTTCAGACATCTGATGAGAGATTCTTTAAACAGCTCCAGCCAG 728
Db 105 GlyIleArgThrGlyPheLeuLysIleLeuArgLysIleMetArgAsnPheSerAspLeuArg 124
OY 729 AAGCTGCTCGGAAAAGATGGGTCCACTGCCACGCTGTCTTCGGCTGTAGACAAATTCTT 788
Db 125 AenGluMetAspArgSerGlySerThrHisAlaValAlaGluMetIleSerProLysHisIle 144
OY 789 TATATTTCGCAACCTCGAGAGATATGTCGGGCAATCTTGCTGTATATGAGAGAGATCA 848
Db 145 TyrPheIleAsnCysGlyHisPheSerThrAlaValLeuTyrHisAsnGlyGln----- 161
OY 849 AAACATGACAGCTTAAAGCCTCAGCAAAAGACATTAATCAATCTCAGTATGAGACCGATG 908
Db 162 -----ValCysPheSerThrHisAspHisLysProCysAsnProArgGlyLysGlu 178
OY 909 AGGATACAGAAAGCTCGAGAGAAAGCTCAGGATGGCGCTGTTTGGCGCTGCTAAGAGTG 968

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Db      179 ArgIleGlnHemalagLyglYsSerValMetIleGlnArgValAsnGlYSerLeuAlaVal    198
Oy      969 TCACGGCTCCATTGGGGAGCGG3GCAGTACAAGCGGTGCGGT-----1007
Db      199 SerArgAlaLeuGlyAerTyrAerTyrlYlVsCyValAspGlyLysGlyProthrGluGln    218
Oy      1008 ---GTCAACCTCTGTGGCCCCGACATCCAAAGCCTGCCAGCTAACCCCCCAAAGAAGCTTCATT    1066
Db      219 LeuValSerProGluProGluProGluValTyrgluIleLeuArgAlaGluGluSerProlunHele    238
Oy      1065 TTGTGGCGCTGTGAATGGGGGCTCTTCAAGGCTTTTAACCCCGAAGAAGACCGTGAACTTCATC    1124
Db      239 IleuAlaCysAserGlytIetrAapValMetSerAsnGluGluLeuCysGluTyrtAl    258
Oy      1125 TTGTCTGTGTCTCGAAGATGAAAGATCCAGACC CGGGAAGGGAAGTCCGCGACGCCAGCC    1184
Db      259 LysSerThrGluGln-----ValSerAsp    266
Oy      1185 CCGTACAGACAGACGCGCTGCACACAGGCTGGCCCAACAGGCGGTGCACGCGGCTCGGCCAC    1244
Db      267 AspLeuAlaLysValCysAsnThrValAlaAspThrCylsLeuIleLysGlySerThrAsp    286
Oy      1245 AAGCTCACGTGAGTAGTGGTGG    1265
Db      287 AsnMetSerIleValLeuVal    293

RESULT 23
PCT-US02-33723-38
Sequence 38, Application PC/TUS0233723
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BECHA, Shanya D.
APPLICANT: BOROMSKY, Mark L.
APPLICANT: DUGGAN, Brendan M.
APPLICANT: EMERLING, Brooke M.
APPLICANT: FORSYTHE, Ian J.
APPLICANT: GANDHI, Ameena R.
APPLICANT: GORVAD, Ann E.
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: HARPALIA, April U.A.
APPLICANT: KHAN, Farrah A.
APPLICANT: Lal, Preeti G.
APPLICANT: LEE, Ernestine A.
APPLICANT: LEE, Soo Yeun
APPLICANT: LINDQUIST, Erika A.
APPLICANT: LU, Dying Alina M.
APPLICANT: LU, Yan
APPLICANT: MARQUIS, Joseph P.
APPLICANT: NGUYEN, Daniel B.
APPLICANT: ARVIZU, Chandra S.
APPLICANT: RAMKUMAR, Jayarami
APPLICANT: RECIPON, Shirley A.
APPLICANT: RICHARDSON, Thomas W.
APPLICANT: SWARNAKAR, Anita
APPLICANT: TANG, Y. Tom
APPLICANT: THORNTON, Michael B.
APPLICANT: TRAN, Uylen K.
APPLICANT: CHAWLA, Natinder K.
APPLICANT: WARREN, Bridget A.
APPLICANT: YANG, Junming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry
APPLICANT: ZEBARJADIAN, Vaganeh
TITLE OR INVENTION: KINASES AND PHOSPHATASES
FILE REFERENCE: PF-1244 PCT
CURRENT APPLICATION NUMBER: PCT/US02/33723
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/345,474
PRIOR FILING DATE: 2001-10-19

```


D	44	ProAspAlaArgProValaArgSerProAlaArgGlyAArgThrLeuProTrpAsnAlaGly	63
Q	330	-----GAAAGAGAAAAACCTCCGAGAGAAAGAAATGGCACTGAGAGAGCTTGCGAAAAG	386
D	64	TyrAlaGluValIleAsnAlaGluIlySerGlnPheAsnGluAspGlnAlaIaIaCysGly	83
Q	387	AAAGTTTGAAGAGCCTCTCCGATGACTTCTTGGCTGGAAGAGGCTATGTGGCTGAGCGAAG	446
D	84	lyuueCys--IleArgAArgGluPheGlyLe-----	94
Q	447	GGTGAAGAGAGAGATCCAGATGCCACGTATCTGAAACGATCACCGAGAGTGT	506
D	95	-----GlnGlnHisGlnIlyuTrpLeuThrVal-----Cys	104
Q	507	AGGCCCCCATCTCTCCCTCATTAATCTCGGGTTTCATATTTGCTGTTTTGATGACATGGA	566
D	105	-----ProGlnGluPheLeuThrGly--HisTyrTrpAlaLeuPheAspGlyHisGly	121
Q	567	GGAATTCGAGCCTCAAAATTTGCTGCACAGAAATTGCATCAAACTTAACTCAGA-----	620
D	122	GlyProAlaAlaIaIleLeuAlaAlaAsnThrLeuHisSerCysLeuArgArgGlnLeu	141
Q	620	-----	620
D	142	GluAlaValaIaGluGlyMetIleAlaProGlnProPromethiIleuSerGlyArgCys	161
Q	621	-----AAATTTCTTAAAGAGATGTAACTACGTATGAGAGAAAACCGTG	662
D	162	ValCysProSerAspProGlnPheValGluGluIlyGlyIleGlnAlaGluAspLeuVal	181
Q	663	AAGAAGTGGCTTTTGGACACTTTCACACATCACTGATGAAGAATTCCTTAA-----CA	716
D	182	IleGlyAlaLeuGlnAsnAlaPheGlnGluCysAspAspValIleGlyArgGluLeuGln	201
Q	717	GCTTTCAGCCAGAAACCTGCTCGGAAAGATGGGTCCACTGCCAGTGTGTGGCTGTGA	776
D	202	AlaSerGlyGln-----ValGlyGlyCysThrAlaLeuValaIaValPheLeu	217
Q	777	GACACATTTCTTATATTGCTCCAACTCCGAGATAGTCCGGCAATCTGTGTGCTTAAT	836
D	218	GlnGlyIlyuLeuTyrValaIaAsnAlaGlyAspSerAspAlaIleLeuValaArg-----	235
Q	837	GAGAGAGTCAAAAAATGACGAGCCTTAAAGCCTTCAGCAAGAGACATTAATCCAACTCAAT	896
D	236	-----ArgHisGluIleArgGlnLeuSerSerGlnPheThrProGlu-----	249
Q	897	GAAGAGCGATGAGATGCACAGA-----GCTGGA-----	926
D	250	ThrIlyuArgIlaArgIleGlnGlnLeuAlaPheThrTyrProGluLeuAlaGlyGln	269
Q	926	-----	926
D	270	PheThrArgLeuGluPheProArgArgLeuIlyGlyAspAspLeuGlyGlnIlyuValLeu	289
Q	926	-----	926
D	290	PheArgAspHisIleMetArgIlyTrpSerTyrIlyuArgValaGluIlyuSerAspLeuIlyu	309
Q	927	-----GAAAGCTGAGAGATGGGCGCTTTTGGCGCTGACAGAGCTCA	971
D	310	TyrTrpLeuIleHisGlyGlnGlyArgGlnAlaArgLeuLeuGlyThrIleAlaValSer	329
Q	972	CGCTCACTGGGGAGCGGCACTCAAG-----CGCTGGCT	1007
D	330	ArgGlyIlyuLeuIlyAspHisGlnLeuArgValaIleuAspThrAspIleGlnIlyuIlyuProPhe	349
Q	1008	GTCACCTGTGTGCC-----GACATCAAGCGCTGCCCACTGACCCCCAAT	1057
D	350	LeuAsnSerIleProGlnValaThrValaIleuAspValaHisGlnLeuAlaValaGlnGluGln	369
Q	1053	GACAGGTCAATTTGTGTGGCCTGTGATGGGCTTTCAAGGTCTTTTACCCCAAGAAAGCC	1112
D	370	Asp-----ValValaValMetAlaThrAspGlyIlyuTrpAspValaIleuSerAsnGluGlnIlyu	388

Gy	113	GTGAATTATCTTGGTCCTGCTCGAAGATGAAGAAG-----	1148
Db	389	AlLLeuLeuValArgSerPheLeuThrIlyAenGIInLyAspArpProHISArgPheSer	408
Gy	1149	-----ATCCAGACCCGGAAGAAAGTCGCCAGCCGACCGCCGCTAC	1190
Db	409	GlUleuAlaIylMetIleuLeuIleHISanThrGIInLyIylYAsp-----	422
Gy	1191	GAAGCAGCCTGCACAGGCTGCGCAACAAGGGATGCGACGGGGC-----TCGGCCAC	1244
Db	423	-----AanGIyAlaThrIlyGIInLyGIInValSerTyzAsp	434
Gy	1245	AAGCTACTGTGATGCTGTGCTCGGAATAGGGCATCTAGAGGGTGCGCGCCGCTCAGAGAAC	1304
Db	435	AspValASerValPheValITyrProIle---HisSerGIInIaGIInLyIylSerTyzAsp	453

Search completed: February 9, 2003, 18:12:01
Job time : 60.5 secs

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1 FILING DATE:
 2 ATTORNEY/AGENT INFORMATION:
 3 NAME: BILLINGS, LUCY J.
 4 REGISTRATION NUMBER: 36,749
 5 REFERENCE/DOCKET NUMBER: PF-0470 US
 6 TELECOMMUNICATION INFORMATION:
 7 TELEPHONE: 650-855-0555
 8 TELEFAX: 650-845-4166
 9 TELEX:
 10 INFORMATION FOR SEQ ID NO: 2:
 11 SEQUENCE CHARACTERISTICS:
 12 LENGTH: 392 amino acids
 13 TYPE: amino acid
 14 STRANDEDNESS: single
 15 TOPOLOGY: linear
 16 IMMEDIATE SOURCE:
 17 LIBRARY: KIDN0102
 18 CLONE: 195647
 19 US-09-013-881-2

Alignment Scores:	
Pred. No.:	9.02e-200
Score:	100.00%
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Best Match:	78.83%
DB:	4
length:	332
Matches:	332
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-935-124A-1 (1-1422) x US-09-013-881-2 (1-392)

[illegible]

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OY 762 TGTSTTCGGCTGAGACAACTTCCTTTATATGCGCAACTCTGGAGATGTGTGGGCAATC 821
Db 221 CysValLeuAlaValAspAsnIleLeuYrIleAlaAsnLeuGlyAspSerArgAlaIle 240
OY 822 TTGTGTGTTATTAATGAGAGAGACTCAAAAAACATGCAGCCTTAAGCCTCAGCAAAAGCAT 881
Db 241 LeuCyArgTyrAsnGlnGlnSerGlnYsHleAlaIleuSerIleuSerIleGlnHis 260
OY 882 AATCCAACTCAAGTATGAAAGCGCGAGATGATGCAGAAAGCTGAGAAAGCTCAGGAT 941
Db 261 AsnProThrGlnTyrGlnGlnArgMetArgIleGlnYsAlaGlyeYAsnValArgAsp 280
OY 942 GAGCGCTTTTGGGCGGCTGAGAGGTGCACGCTCCATTGGGGAGACGGGCGATGCAACGCG 1001
Db 281 GlyArgValLeuGlyValLeuGlnValSerArgSerIleGlyAspGlyGlnTyrIleArg 300
OY 1002 TGGCGTGCACCTCTGTGCGCCGACATCAGACGCTGCAGCTGACCCCAATGACAGTTTC 1061
Db 301 CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
OY 1062 ATTTGTGTGGCCCTGTATGGAGGCTCTTCAAGGCTTTAACCAGAAAGACCGCTGAATTC 1122
Db 321 IleLeuLeuAlaCysAspGlyLeuPheIleYsValPheThrProGlnGlnAlaValAsnPhe 340
OY 1122 ATCTTGCTCGTCTCGAGGATGAAAGATCCAGACCCGGGAGAGGAAGTCCGACCGAC 1181
Db 341 IleLeuSerCysLeuGlnArgGlnArgIleGlnThrArgGlnGlyLysSerIleAlaAsp 360
OY 1182 GCCCGCTACAGACGACGCTTCCAAACAGGCTGGCCCAACAGACCGCTGCAGCGGCGCTCGCC 1241
Db 361 AlaArgTyrGlnAlaIleAlaCysAsnArgLeuAlaAsnLysAlaIleAlaGlnArgIleSerAla 380
OY 1242 GACAACGTCACTGATGTGTGTGGTGGGAGATGAGGCGAC 1277
Db 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 2
US-08-822-701-8
: Sequence 8, Application US/08822701
: Patent No. 5976853
: GENERAL INFORMATION:
: APPLICANT: Guthridge, Mark
: APPLICANT: Basillco, Claudio
: TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
: TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/822,701
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-I-002 N
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:

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/ LENGTH: 306 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus
/ US-08-822-701-8

Alignment Scores:
Pred. No.: 1,66e-26 Length: 306
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 48
DB: Gaps: 12

US-09-935-124a-1 (1-1422) x US-08-822-701-8 (1-306)
QY 417 GGTCTGAAGGCTATGCTGCTGAGCGGAGGAGGAGGAGATGCGAGATGCCAC 476
DB 21 GlyLeuArgTyrGlyLeuSerMetGlnGlyTyrPargValGluMetGluAspAlaHis 40
QY 477 GTCACTCTGAACGATCACCGAGAGGTGATGAGCCCGCATGCTCCCTATTAATCTGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---Trp 53
QY 537 TCATATTTTGTCTGTTTGTATGACATGAGAAATTCAGACCTCAAAATTTGCTGCACAG 596
DB 54 SerPheHehAlaValTyrAspGlyHisAlaGlySerGlnAlaAlaTyrTyrCysGlu 73
QY 597 AATTGCATCAAACTTAATCAGAAATTTCTT---AAAGAGAT---GTATCACT 647
DB 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLeuGlySerAlaGlyAlaPheSer 93
QY 648 GTAGAGAAACCTGTAAGAGATGCTTTTGGACATTTCAAGCATCTGATGAAGATTC 707
DB 94 ValGlu---AsnValIleYsAsnGlyLeuArgThrGlyPheLeuGluIleAspGluHisMet 112
QY 708 CTTAAACAGCTCTCCAGAGATGCTGTAAGAGATGCTGTAAGAGATGCTGCTGCTGTT 767
DB 113 ArgValMetSerGluIleYsHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTGAGCAACATCTTTATATGCAACCTCGAGATGTCGGGCAATCTTGCT 827
DB 133 LeuIleSerProGlnHisThrTyrThrIleAsnGlyAspSerArgGlyLeuLeuGly 152
QY 828 CTTTATATGAGAGAGCTCAAAACATGACGCTTAAGCCTCAGCAAGAGATATGCCA 887
DB 153 Arg-----AsnArgIleYsValHisPhePheThrGlnAspHisIleYsPro 166
QY 888 ACTCAGTATGAAGCCGATGAGATACAGAAAGCTGAGAGAAACCTCAGAGATGGGCT 947
DB 167 SerAsnProLeuGluIleYsGluArgIleGlnAsnAlaGlyIleSerValMetIleGlnArg 186
QY 948 GTTTTGGCGCTGTAAGAGGTGTCACGCTTCATTGGGAGCGGAGATCAAGCGCTGC--- 1004
DB 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrIleYs---CysVal 205
QY 1005 -----GGTGTACCC-----TCTGTGCCCGACATCAGA 1031
DB 206 HisGlyIleGlyProThrArgGluIleValSerProGluIleValHisAspIleGlu 225
QY 1032 CGCTGCAGCTGAGCCCGCATGACAGATTCATTTTGTGCTGTGATGGGCTCTTCAAG 1091
DB 226 ArgSerGlu-----GluAspArgGlnPheIleIleLeuAlaCysAspGlyIleTyrAsp 243
QY 1092 GTCTTTACCCGAGAGAGCGGAGATTCATCTGCTGCTGCAG-----GATGAA 1145
DB 244 ValMetGlyAsnGluGluLeuGlyAspPheValArgSerArgLeuGluValThrAspAsp 263

RESULT 3
US-08-935-855-8
/ Sequence 8, Application US/08935855
/ Patent No. 6086485
/ GENERAL INFORMATION:
/ APPLICANT: Galtridige, Mark
/ APPLICANT: Basilico, Claudio
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, PIN13
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ STREET: Floor
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/935,855
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq, David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 306 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus
/ US-08-935-855-8

Alignment Scores:
Pred. No.: 1,66e-26 Length: 306
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 48
DB: Gaps: 12

US-09-935-124a-1 (1-1422) x US-08-935-855-8 (1-306)
QY 417 GGTCTGAAGGCTATGCTGCTGAGCGGAGGAGGAGATGCGAGATGCCAC 476
DB 21 GlyLeuArgTyrGlyLeuSerMetGlnGlyTyrPargValGluMetGluAspAlaHis 40
QY 477 GTCACTCTGAACGATCACCGAGAGGTGATGAGCCCGCATGCTCCCTATTAATCTGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---Trp 53
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QY 537 TCATATTTGCTGCTTTTGTGATGAGCATGAGAAATTCGAGCCTCAAAATTTGCTGCACAG 596
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Db 54 SerPhePheAlaValIyrAspGlyHleAlaGlySerGlnValAlaIytrCyseGln 73
QY 597 AATTTCGATCAAAACTTAATCAGAAAAATTTCTCT--AAAGGAGAT-----GTAATCACT 647
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 HleLeuLeuAspHleIleThrAsnAsnGlnAspPheIleGlySerAlaGlyAlaProSer 93
QY 648 GTAGAGAAAAACCGTGAAGAGATGCTTTTGTGACACTTTCAAGCATGATCTGTAAGAGTTTC 707
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 94 ValGlu---AsnValIyAsnGlyIleArgThrGlyPheLeuGlnIleAspGlnHleSmet 112
QY 708 CTTAAACAGCTTCCAGCCAGAAAGCTGCTGGAAGATGGTCACTGCCAGCTGTGT 767
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 ArgValIeSerGlnIyIySerGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCGGTAGACAACTTCTTTATTTATGCCACCTGGAGATGTGGGCAATCTTGTGT 827
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 LeuIleSerProGlnIleThrTyIyrPheIleAsnCyseGlyAspSerArgIyLeuLeuCyS 152
QY 828 CATTATATGAGAGAGTCAAAAACATGACGCTTAAGCCTCAGCAAGAGCATTAATCCA 887
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 Arg-----AsnArgIyIyValHlePhePheThrGlnAspHleSlyIyPro 166
QY 888 ACTCACTATGAAGAGCGAGATGAGGATACAGAAAGCTGAGAGAAACCTCAAGGATGGCGGT 947
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 167 SerAsnProLeuGlnIyIySerGlyAlaGlnAsnAlaGlyIySerValIeMetIleGlnArg 186
QY 948 GTTTGGGCGGTGTAGAGGTGTACCTCCATTTGGGAGCGGAGATACAAAGCCCTGC--- 1004
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspIyIyS---CySVal 205
QY 1005 -----GGTGTCAAC-----TCTGTGCCCGGACATCAGCA 1031
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 HleGlyIyIyGlyProThrGlnLeuValSerProGlnIyValHleSapIleGln 225
QY 1032 CCGTCCAGCTGACCCCAATGACAGTTTCATTTGTGGCTGTAGAGGCTCTTCAAG 1091
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226 ArgSerGlu-----GluAspArgGlnPheIleIleLeuAlaCyAspArgIyIleTyrAsp 243
QY 1092 GTCTTTATCCCAAGAAAGCCGTGAACCTTCATTTGTCTGTCTGCAG-----GATGAA 1145
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 ValMetGlyAsnGlnIyLeuCyAspPheValArgSerArgLeuIyValThrAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACGCCGCTACAGAGAGAGCTGCACAC 1205
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 264 -----LeuGlnIyIyValCyAsn 269
QY 1206 AGCGTGGCCAAAGAGCGGTGCAGCGGCGCTCGGCCGACACCTCACTGTATGTGTGTG 1265
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 270 GluValIyAspThrCyseLeuTyIyIySgIySerArgAspAsnMetSerValIleLeuIle 289

RESULT 4
US-09-206-646-4
; Sequence 4, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Gold, Surya K.
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1 Div
; CURRENT APPLICATION NUMBER: US/09/206,646
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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```

; NAME/KEY: misc_feature
; OTHER INFORMATION: ID No. 6436637 9452526
US-09-206-646-4

Alignment Scores:
Pred. No.: 5,36e-25 Length: 390
Score: 326.00 Matches: 98
Percent Similarity: 45.87% Conservative: 52
Best Local Similarity: 29.97% Matches: 121
Query Match: 12.73% Indels: 56
DB: 4 Gaps: 10

US-09-935-124A-1 (1-1422) x US-09-206-646-4 (1-390)
QY 333 AAGAGAAAACCTCCAGAGAAAGAAATGGCAGGAAAGACTTGTGAAAAAGAAATT 392
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LysProIyIyThrGlnIyAsnHleAsnAlaHleSgIyAlaGlyAsn----- 20
QY 393 TGTAAAGCTCTTCGGATCTTTGTGATGAGAGGCTATGTGGCTGAGCGGAAGGTGAG 452
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 -----GlyLeuArgTyIyGlyLeuSerSerMetGlnIyTyr 32
QY 453 AGGAGAGATGACAGATGCCACGTCATCTGAACGACATCACGAGAGGTAGGCC 512
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 ArgValIyGluMetGluAspAlaHleThrAlaValIyGlyIle----- 46
QY 513 CGATGTCCTCATTAATCCGGTTCAATTTGTGCTTTTGTGATGACATGAGGAATT 572
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 47 ProHleGlyLeu---AspAsnTyrSerPhePheAlaValTyIyAspGlyHleAlaGlySer 65
QY 573 CGAGCCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTA-----ATC 617
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 ArgValAlaIleAsnTyIyCyseSerThrHleLeuLeuGlnHleIleThrAsnGlnAspPhe 85
QY 618 AGAAAATTTCTTAA--GGAGATGTAATC-----AGTGTGAGAAAACCTGAAAGCA 668
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 86 ArgAlaAlaAspIySerGlySerAlaLeuGlnProSerValGln---SerValIyIyThr 104
QY 669 TGCCTTTGGACACTTTCAGCATCTGTAGTGAAGAGTTCTTAAACAGCTTCCAGCCAG 728
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 105 GlyIleArgThrGlyPheLeuIyIleAspGlnIyIyMetAspAsnPheSerAspLeuArg 124
QY 729 AAGCTGCTCGGAAGAGATGGGTCACTGCACGTGTGTCTGCTGTAGACAACTTCT 788
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 AsnGlyMetAspArgSerGlySerThrAlaValIyValIeMetValSerProThrHleSmet 144
QY 789 TATATTGCCAATCTCGAGATATGTGGGCAATCTTGTCTGTTATATGAGAGAGTCAA 848
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 TyIyrPheIleAsnCyseGlyAspSerArgAlaValIleuCyAspArgAsnGlyGln----- 161
QY 849 AAACATGACGCTTAAGCCTCAGCAAGAGCATTAATCCAACTCACTATGAAAGAGCGGATG 908
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 162 -----ValCyPheSerThrGlnAspHleSlyIyProCyAsnProValGlnIySgIy 178
QY 909 AGGATACAGAAAGCTGGAAGAAAGTCAAGGATGGCGTGTGTGGCTGTAGAGGTG 968
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 ArgIleGlnAsnAlaGlyIyIySerValIeMetIleGlnArgValAsnGlySerLeuAlaVal 198
QY 969 TCAGCCTCCATTGGGAGCGGAGCAATCAAGCGCTGCGGT----- 1007
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 199 SerArgAlaIleuGlyAspTyIyAspTyIyCySValAspGlyIyGlyProThrGln 218
QY 1008 ---GTCACCTCTGTGCCGACATCAGAGCTCCAGCTGACCCCAATGACAGTTCATT 1064
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 219 LeuValIySerProGlnIyProGlnValIyIyGlnIyValIyArgAlaGlnIyAspIyIyVal 238
QY 1065 TTGTTGGCTGTGATGGGCTCTTCAAGGCTTTTACCCAGAAAGAGCCGTGAATCTTCAT 1124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 ValLeuAlaCyAspGlyIyIleTyrAspValIeMetSerAsnGlnIyLeuCySgIyIyHleVal 258
QY 1125 TTGTCTGTCTTGAGAGATGAAAGATCCAGACCCGGAGAGGAGATCCGACGCCAGCC 1184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 259 LysSerArgLeuGln-----ValSerAsp 266

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QY      1185 CGCAGCAACGACCGCCGAAGAAGCGGTGGCCAAACAAGCGGCGCTCGAGCCGAC   1244
Db      267 AepLeuLuanValCYAsnITTPValVaLaephTrCySLeuHtIbLYgLySerArGaAp   286
QY      1245 AACCTCACTGTATGAGTGCTG 1265
Db      287 AmMetSeValValLeuVal 293

RESULT 5
US-08-822-701-7
; Sequence 7, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basillco, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATE:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-343-1684
; TELEFAX: 201-487-5800
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 309 amino acids
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus

US-08-822-701-7

Alignment Scores:
Pred. No.:          1,72e-24           Length:          309
Score:              320.50             Matches:          98
Best Local Similarity: 46.06%          Conservative:     54
Query Match:        29.70%             Mismatches:     115
DB:                 12.52%             Indels:         63
                               Gaps:         12

US-09-935-124A-1 (1-1422) X US-08-822-701-7 (1-309)
QY      333 AAAGAGAAAAGCTCCGAGCAAGAGAAAGATGCAGTGAAGACTTTGTGAAAAAGAAAGTT 392
Db      7    LyeTroLyshThGlUyVShIsamAlahISelYAladLYAn----- 20
QY      393 TGTAAAGCCTTCGCGTAATCTTGTGCTCGAAGGCTATGTGCTCGAACGGAAGGCTAG 452
Db      21 -----GlyLeuNryrGLyLeuSeSerMetcGlnGLyTP 32

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/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ STREET: Floor
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/935,955
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 309 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: Mus musculus
/
US-08-935-855-7

Alignment Scores:
Pred. No.: 1,72e-24 Length: 309
Score: 320.50 Matches: 98
Percent Similarity: 46.06 Conserved: 54
Best Local Similarity: 29.704 Mismatches: 115
Query Match: 12.524 Indels: 63
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-08-935-855-7 (1-309)
QY 333 AAGAGAAAACCTCCGAGAGAGAAATGCGAGTGAAGAGCTTGTGAAAAAAGTT 392
DB 7 LysProIythrGluYshIshAenAlahIsgLYAlaGlyAen----- 20
QY 393 TGTAAAGCTCTTGGTGATCTTTGGTGAAGGGCTATGTGAGCGGAGGGTGAG 452
DB 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyr 32
QY 453 AAGGAGGAGATGCGAGATGCCCGCTGATCTGACGACATCCAGAGAGGTGAGCCC 512
DB 33 ArgValaGluMetGluAspAlaHisThrAlaValaGlyIle----- 46
QY 513 CCATGCTCCCTATTAATCTGGGTTGATATTTGATTTTGTGATGAGATGAGGAATT 572
DB 47 PtoHsGlyLeu---AspAsnTyrSerPhePheAlaValaTyrAspGlyHisAlaGlySer 65
QY 573 CGAGCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTA-----ATC 617
DB 66 ArgValaAlaAsnTyrCySerSerThrHisLeuLeuGlnHisIleThrThrAsnGluAspPhe 85
QY 618 AAAAAATTTCTTAA--GAGAGTGAATC-----AGTGTAGAG-----AAAACGCG 662
DB 86 ArgAlaAlaAspIySerGlySerAlaLeuGluProSerValaGluSerValaGlyThrGly 105
QY 663 AAGAGATGCTTTTGGACACTTTCAGCATACGATGAGGAAGTTCTTAAACAAGCTTCC 722
DB 106 ArgThrGlyPheLeuYsIle-----AspGluTyrMetArgAsnPheSer 120

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QY 723 AGCCGAAGCTGCTCG--AAAGATGGGTCCACTGCCACGCTGTCTTGGCTGTAGC 779
DB 121 AspLeuArgAsnGlyMetAspArgSerGlySerThrAlaValaGlyValMetValSerPro 140
QY 780 AACATTTTATATATGCCAAGCTCGAGATAGTCCGGCAATCTTGTGCTTATATAG 839
DB 141 ThrHisMetTyrPheIleAsnCySerGlyAspSerArgAlaValaLeuCyAspArgAsnGlyGln 160
QY 840 GAGAGTCAAAAATGATGACGCTTAAGCTTCAGCAAGAGCATTAATCAAGTATGAA 899
DB 161 -----ValCySerPheSerThrGlnAspHisLeuProCyAsnProVal 174
QY 900 GAGCGAATGAGATACAGAAAGCTGAGAGAAAGTTCAGGATGGCGTGTGTTGGGCGTG 959
DB 175 GluYsgIuArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValaAsnGlySer 194
QY 960 CTNAGGTGTACCGCTCCATTGGGAGCGGCGAGTCAAGCGCTGGCGGT----- 1007
DB 195 LeuAlaValSerArgAlaLeuGlyAspTyrAspTyrLysCyValaAspGlyLysGlyPro 214
QY 1008 -----GTCACTCTGTGCGCCGATCATCAGACGCTGCACGCTGACCCCAATGAC 1055
DB 215 ThrGluGlnLeuValSerProGluProGluValTyrGluIleValaIArgAlaGluAsp 234
QY 1056 AGTTCATTGTTGCTGCTGTGATGGCTCTTCAAGGCTTTTACCCAGAAAGACCGCTG 1115
DB 235 GluPheValValLeuAlaCyAspGlyIleTyrAspValMetSerAsnGluGluLeuCyS 254
QY 1116 AACTTCATCTTCTCTGTCTGAGATGAAAAGATCCAGACCCGGGAAAGGAAGTCCGA 1175
DB 255 GluPheValLysSerArgLeuGlu----- 262
QY 1176 GCCGACGCCCGCTCAAGACAGCTGCAACAGCTGCGCCAAACAGGCGGTGACGGGCG 1235
DB 263 ValSerAspAspLeuGluGlnAsnValCyAsnTyrValaAspThrCyLeuHisIsgly 282
QY 1236 TCGGCCGACACAGCTCATGTGATGGTGTG 1265
DB 283 SerArgAspAsnMetSerValValLeuVal 292

RESULT 7
US-08-873-093-3
/ Sequence 3, Application US/08873093
/ Patent No. 5853997
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Zhang, Hong
/ TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: Pasteo for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/873,093
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749

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Db 66 ArgValAlaIaenTyrCySerThrHnSLeuLeuGlnHisIleThrThraSngIuaSrpHe 85
Qy 618 AGAAATTTCTTAAGAGAGATGTAATC-----AGTGTAGAGAAAACCGTAGAGAG 668
Db 86 ArgAlaAlaIaAspIysSerGlyPheAlaLeuGlnProSerValGlu---AsnValIlyThr 104
Qy 669 TGCCTTTTGGACATTTCAAGCACTACTGATGAAGAATTCCTTAACAGCTTCCAGCCAG 728
Db 105 GlyIleArgThrGlyPheLeuIlySileAspGlyTyrMetArgSnpHesSerLeuArg 124
Qy 729 AGCCGCGCTGGAAGAATGAGTGCACAGCTGCTTGGCTGTGATGACAACTTTCTT 788
Db 125 AsnGlyMetAspIrgSerGlySerThrAlaValGlyValMetIleSerProThrHisIle 144
Qy 789 TATATTGCCAACTCCGAGATAGTCCGGCAATCTTGTCGTTATATGAGAGAGTCAA 848
Db 145 TyrPheIleAsnCySerGlyAspSerAlaValLeuCyAspIrgSngIyn-----161
Qy 849 AAACATGACAGCTTAAGCTTACACAAAGACATATCCAACTGATGAGAGCGGATG 908
Db 162 -----ValCySrpHesSerThrGlnAspHisIlySProCyAspIrgPrometGlnIlySgln 178
Qy 909 AGGATACAGAAAGCTGAGAGAAACGTCAGGAGATGGCGCTTTTGGCGCTTACAGCTG 968
Db 179 ArgIleGlnAsnIleArgIlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
Qy 969 TCACGCTCCATTTGGGAGCGGAGTACAGCGCTGCGGT-----1007
Db 199 SerArgAlaLeuGlnIlyAspIryAspIryIlySryCyValAspIlySngIyProThrGln 218
Qy 1008 ---GTACCTCTGTGCTCCGACATCAAGCTGCGACCTGACCCCAATGACAGTTTCATT 1064
Db 219 LeuValSerProGlnProGlnValTyrGlnIleLeuArgIleGlnIlyAspIrgIlyPheVal 238
Qy 1065 TTGTTGGCGCTGATGGGCTCTTCAAGCTTTTACCCCAAGAAACCGGAACTTCATC 1124
Db 239 ValLeuAlaCyAspIryIleIrrPaAspValMetSerAsnGlnIlyLeuCySngIlyPheVal 258
Qy 1125 TTGTCTGTCTCGAGATGAAAGATCCAGACCCGGAAAGGAAGTCCGACCGCAGCC 1184
Db 259 AsnSerArgLeuGln-----ValSerAsp 266
Qy 1185 CGGTACGAAGACGCTTCAACAGGCTGGCCACAGGCGGTGACCGGCTTGGCGGAC 1244
Db 267 AspLeuGlnAsnValCyAsnThrValIlyAspThrCyLeuHisIlySngIySerArgAsp 286
Qy 1245 AACGTACCTGTATGTGTGTG 1265
Db 287 AsnMetSerIleValLeuVal 293

RESULT 9
US-08-822-701-9
Sequence 9, Application US/08822701
Patent No. 597853
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/822,701
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jackson Esq., David A.
;/ REGISTRATION NUMBER: 26,742
;/ REFERENCE/DOCKET NUMBER: 1049-1-002 N
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 201-487-5800
;/ TELEFAX: 201-343-1684
;/ INFORMATION FOR SEQ ID NO: 9:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 281 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ HYPOTHEICAL: NO
;/ FRAGMENT TYPE:
;/ ORIGINAL SOURCE:
;/ ORGANISM: Saccharomyces cerevisiae
;/
US-08-822-701-9
Alignment Scores:
Pred. No.: 3,32e-24 Length: 281
Score: 317.50 Matches: 95
Percent Similarity: 45.87% Conservative: 44
Best Local Similarity: 31.35% Mismatches: 93
Query Match: 12.40% Indels: 71
DB: Gaps: 12
US-09-935-124A-1 (1-1422) x US-08-822-701-9 (1-281)
Qy 432 GTGGCTGAGCGGAAGGAGAG-----AGGAGAGATGACAGATCCCACTCATCTG 485
Db 23 ValAlaGlnAsnIleAspSerIlyAspPheArgThrMetGlnAspValHisThrTyrVal 42
Qy 486 AACGACATCACCGAGAGAGTGTAGCCCCCATGCTCCCTATTACTCGGGT-----TCA 539
Db 43 LysAsnPheAla-----SerIrgLeuAspIrgIly 52
Qy 540 TATTGTGCTGTTTGTATGACATGAGAGAAATTCAGCCTCAAAATTTGCTGCACAGAT 599
Db 53 TyrPheAlaValPheAspIryHisIleGlyIleGlnIleAspIryProSngIySngHis 72
Qy 600 TTGCAT-----CAAACTTAATCAGAAAATTTCTTAAGAGATTAATCACT 647
Db 73 LeuHisThrIleIleGlnGlnAsnIleLeu-----AlaAsp 84
Qy 648 GTAGAGAAAACGTTGAGAGATGCTTTTGGACATTTCAAGCATATGATGAGAGTTC 707
Db 85 GlnThrArgAspValArgAspValLeuAsnAspSerPheLeuAlileAspIrgIlyIle 104
Qy 708 CTTAAACAAGCTTCCAGACGAGCTGCTGCGGAAGAATGGTTCAT---GCCAGTGT 764
Db 105 -----AsnThrIlySngIyValGlnAsnSerGlyCyThrAlaIleValCyS 119
Qy 765 GTTCTG-----GCTGTAGACAACAT-----785
Db 120 ValLeuArgIrgIlyLeuProAspSerValSerAspSerMetAspLeuAlaGlnHis 139
Qy 786 -----CTTATATTGCCAACTCCGAGATAGTCCGGCAATCTGTGCTGTTATAT 836
Db 140 GlnArgIlySngIyThrAlaAsnValGlyAspSerArgIleValLeuPheArgSngIy 159
Qy 837 GAGAGAGTCAAAAACATGACGCTTAAGCCTTACACAAAGACATATCCAACTGAGAT 896
Db 160 Asn-----SerIleArgLeuThrTyrAspHisIlyAlaSerAspThr 173
Qy 897 GAAGACCGATGAGATACAGAAAGCTGAGAGAAACGTCAGGAGATGGCGGTGTTGGGC 956
Db 174 LeuGlnMetGlnArgValGlnGlnIleGlyIlyLeuIleMetIlySerArgValAsnGly 193

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QY 957 GTGCTAAGGTCTACGCTTCATTGCGGAGCGGAGTACAAAGCGCTGCGTGCACCTCT 1016
Db 194 MetleuAlaValThrArgSerIeuGlyAspLysPheAspSerLeuValValGlySer 213
QY 1017 GTGCCGACATCAGACGCTGACGCTGACCCCAATGACAGGTTCAATTTTGCGCTGT 1076
Db 214 --ProPheThrThrservAlGluIleThrserGluAspLysPheLeuIleLeuAlaCys 232
QY 1077 GATGGCTCTTCAAGGCTCTTTACCCAGAAAGAGCGTGAACCTTCATCTTCCTGTCTC 1136
Db 233 AspGlyLeuTrpAspValIleAspAspGlnAspAlaCysGluLeuIleLysAspIleThr 252
QY 1137 GAGGATGAAAGATCCAGACCCGGAGAGGAGTCCGACGCCGACCGCTACGAAGCA 1196
Db 253 GluProAsnGlu----- 256
QY 1197 GCGTCGAACAGCGTGGCCCAACAGCGGCTGACGCGGCGTCCGCGCCGACAGCTGCTG 1256
Db 257 AlaAlaLysValLeuValArgTyrAlaLeuGluAsnGlyThrThrsPheAsnValThrVal 276
QY 1257 ATGCTGTG 1265
Db 277 MetValVal 279

RESULT 10
US-08-935-855-9
Sequence 9, Application US/08935855
Patent No. 6066485
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-935-855-9

Alignment Scores:

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Pred. No.: 3,32e-24 Length: 281
Score: 317.50 Matches: 95
Percent Similarity: 45.87% Conservative: 44
Best Local Similarity: 31.35% Mismatches: 93
Query Match: 12.40% Indels: 71
DB: 3 Gaps: 12

US-09-935-124a-1 (1-1422) x US-08-935-855-9 (1-281)
QY 432 GTGGCTAGCGGAGGAGTACG-----AGGAGGAGATGCGAGATGCCACGTCACCTC 485
Db 23 ValAlaGluAsnLysAsnSerLysPheArgThrMetGluAspValHisThrTyrVal 42
QY 486 AACGACATCACGAGAGGTATGCCCCCATCGCCCTTATTCCTGGGTT-----TCA 539
Db 43 LysAsnPheAla-----SerArgLeuAspTrpGly 52
QY 540 TATTTGCTGTTTNTGATGAGATGAGATTTGAGCTCAAAATTTGCTGCACAGAT 599
Db 53 TyrPheAlaValPheAspGlyHisAlaGlyIleGlnLysSerLysTrpGlyHis 72
QY 600 TTGCAT-----CAAACTTAATCAGAAAATTTCTTAAGAGATTAATCACT 647
Db 73 LeuHisThrIleIleGluGlnAsnIleLeu-----AlaAsp 84
QY 648 GTAGAGAAAACGTGAAGAGATGCTTTTGACACTTTCAGACATACGTAGACATTC 707
Db 85 GluThrArgAspValArgAspValLeuAsnAspSerPheLeuAlaIleAspGluIle 104
QY 708 CTTAAACACCTTCACGACGAGAGCTGCTCGAAGAGATGGTCACT---GCCACGTGT 764
Db 105 -----AsnThrLysLeuValGlyAsnSerGlyCysThrAlaIleValCys 119
QY 765 GTTCTG-----GCTGACGACACAT----- 785
Db 120 ValLeuArgTrpGluLeuProAspSerValSerAspSerMetAspLeuAlaGlnHis 139
QY 786 -----CTTATATTCGCACTCGAGATGAGATGCGGACATCTTGCTGTTATAT 836
Db 140 GlnArgLysLeuTrpThrAlaAsnValGlyAspSerArgIleValLeuPheArgAsnGly 159
QY 837 GAGGAGATCAGAAAACATGACCTTAAGCTCGCAAGAGATATTCACATCAAGAT 896
Db 160 Asn-----SerIleArgLeuThrLysPheIleAlaSerAspThr 173
QY 897 GAAGCGGATGCGATACAGAAAGCTTGAGAGAAAGCTCAGGATGGCGTGTGGGC 956
Db 174 LeuGluMetGlnArgValGluGlnAlaGlyLysLeuIleMetLysSerArgValAsnGly 193
QY 957 GTGCTAAGGTCTACGCTTCATTGCGGAGCGGAGTACAAAGCGCTGCGTGCACCTCT 1016
Db 194 MetleuAlaValThrArgSerIeuGlyAspLysPheAspSerLeuValValGlySer 213
QY 1017 GTGCCGACATCAGACGCTGACGCTGACCCCAATGACAGGTTCAATTTTGCGCTGT 1076
Db 214 --ProPheThrThrservAlGluIleThrserGluAspLysPheLeuIleLeuAlaCys 232
QY 1077 GATGGCTCTTCAAGGCTCTTTACCCAGAAAGAGCGTGAACCTTCATCTTCCTGTCTC 1136
Db 233 AspGlyLeuTrpAspValIleAspAspGlnAspAlaCysGluLeuIleLysAspIleThr 252
QY 1137 GAGGATGAAAGATCCAGACCCGGAGAGGAGTCCGACGCCGACCGCTACGAAGCA 1196
Db 253 GluProAsnGlu----- 256
QY 1197 GCGTCGAACAGCGTGGCCCAACAGCGGCTGACGCGGCGTCCGCGCCGACAGCTGCTG 1256
Db 257 AlaAlaLysValLeuValArgTyrAlaLeuGluAsnGlyThrThrsPheAsnValThrVal 276
QY 1257 ATGCTGTG 1265
Db 277 MetValVal 279

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RESULT 11
US-08-873-093-1
/ Sequence 1, Application US/08873093
/ Patent No. 5853997
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goll, Surya K.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Zhang, Hong
/ TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/873,093
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0319 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 478 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: TRIP1LB01
/ CLONE: 13177
/ US-08-873-093-1

Alignment Scores:
Pred. No.: 1,33e-23 Length: 478
Score: 313.00 Matches: 94
Percent Similarity: 44.654 Conservative: 52
Best Local Similarity: 28.754 Mismatches: 125
Query Match: 12.238 Indels: 56
DB: 2 Gaps: 8

US-09-935-124A-1 (1-1422) x US-08-873-093-1 (1-478)
QY 333 AAGAGAAAACCTCCGAGAGAAAGAAATGCGAGTGAAGAGCTTGCGAAAAAAGTT 392
DB 7 LysPrcIySthrGluYshIsaenIahIsGlyAlaGln----- 20
QY 393 TGTAAAGCCTCTTCGGTGAATCTTTGGTCTGAAGCGCTATGCTGAGCGGAGGCTGAG 452
DB 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyr 32
QY 453 AAGGAGAGATGAGATGCCACGTCATCTGACAGCATCACCGAGAGGTGAGGCC 512
DB 33 ArgValGluMetGluSerAlaHisThrAlaValAlaGlyLe----- 46
QY 513 CCATGCTCCCTCATTTACTCGGCTTATATTTGCTGCTTTTATGAGACATGAGGAATT 572
DB 47 ProHIsGlyLeu---GluSerTyrSerPhePheAlaValTyrAspGlyHisAlaGlySer 65
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QY 573 CGAGCCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTAATCAGA----- 620
DB 66 ArgValAlaAsnTyrCysSerThrHisLeuGlnHisIleThrHisAsnGluSerPhe 85
QY 621 -----AAATTTCTTAAAGAGATGTATACATGCTGTGAGAAAAACCTGAAGAGA 668
DB 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGlnLeuSerValGln---AsnValIysAsn 104
QY 669 TGCCTTTGACACTTTCAGCATCTAGTGAAGAGTTCTTAAACAAGCTTCCAGCCAG 728
DB 105 GlyIleArgThrGlyPheLeuLysIleAspGlnTyrMetArgAsnPheSerLeuArg 124
QY 729 AAGCTGCTGGAAGATGGCTCCACTGCGACGTCGTGTTGCTGGCTGTGACAACTTCT 788
DB 125 AsnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetIleSerProIshisIle 144
QY 789 TATATTGCCAATCTGAGATATGTGGGCAATCTTGTCTTATTAATGAGAGAGTCA 848
DB 145 TyrPheIleAsnCysGlyAspSerArgAlaValLeuTyrArgAsnGlyGln----- 161
QY 849 AAACATGACGCTTAAGCCTCAGCAAGCATATTCACACTCACTATGAAAGAGCGGATG 908
DB 162 -----ValCysPheSerThrGlnAspHisLysProCysAsnProArgGlnLysGln 178
QY 909 AAGATACAGAAAGCTGAGAGAAACGTCAAGGATGGCGCTGTTGGCGCTGTAAGGTG 968
DB 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
QY 969 TCACGCTCATTTGGGAGCGGCGAGTACAAAGCCTCGGT----- 1007
DB 199 SerArgAlaLeuGlnLysAspTyrAspTyrLysCysValAspGlyLysGlyProThrGln 218
QY 1008 ---GTCACCTGTGCTCGGACATCAGACGCTCCAGCTGACCCCAAGAAAGACGTTCAAT 1064
DB 219 LeuValSerProGluProGluValTyrGluIleLeuAlaGlnGluSerLysPheIle 238
QY 1065 TTGTTGGCTGTGATGGCTCTTCAAGGCTTTACCCAGAAAGACCGGTGAATTCATC 1124
DB 239 IleLeuAlaCysAspGlyIleTyrAspValMetSerArgnGlnGluLeuCysGluTyrVal 258
QY 1125 TTGTCCTGCTCTGAGAGTGAAGAAAGATCCAGACCCGGAAAGGAAATCCGACCGCAGCC 1184
DB 259 LysSerArgLeuGln-----ValSerAsp 266
QY 1185 CGCTACGAAGACGCTGCAACAGCTGCGCAACAGGCGGTGACGGGCTCGGCGCAGC 1244
DB 267 AspLeuGlnAsnValCysAsnTyrValValAspThrCysLeuHisLysGlySerArgAsp 286
QY 1245 AACGTCACTGTGATGATGATG 1265
DB 287 AsnMetSerIleValLeuVal 293

RESULT 12
US-08-873-093-4
/ Sequence 4, Application US/08873093
/ Patent No. 5853997
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goll, Surya K.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Zhang, Hong
/ TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS Version 2.0
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873, 093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDBESS: single
TOPOLGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1452526
US-08-873-093-4

Alignment Scores:
Pred. No.: 1,33e-23 Length: 478
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
Gaps: 8

US-09-935-124A-1 (1-1422) x US-08-873-093-4 (1-478)
QY 333 AAGAGAAAACCTCCGAGAGAGAGAGATGCGACGATGAGAGCTTGAGAAAAGAAATT 392
DB 7 LysProlyserThrGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
QY 393 TGTAAAGCCTCTCGGTATCTTTGTCTGAAGGGCTATGTGGCGGAGAGGTGAG 452
DB 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyr 32
QY 453 AGGAGAGATGACAGATGCCACGCTCATCTCTGAACGACATCCAGAGAGGTAGGCC 512
DB 33 ArgValGluMetGluAspAlaHisThrAlaValAlaGlyLe----- 46
QY 513 CCATGTCCTCATTACTCGGGTTTCATATTTTCTGTTGATGAGATGAGGATTT 572
DB 47 ProHisGlyLeu--GluAspTyrPserPhePheAlaValTyrAspGlyHisAlaGlySer 65
QY 573 CGAGCTCAAAATTTGCTGACAGAAATTTGCATCAAACTTAATCAGA----- 620
DB 66 ArgValAlaAsnTyrCysSerThrHisLeuLeuGlnHisIleThrHisGluAspPhe 85
QY 621 -----AAATTTCTTAAGAGAGATGTAATCAAGTATAGAGAAAACCTGAAAGA 668
DB 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGluLeuSerValGlu--AsnValLysAsn 104
QY 669 TGCCTTTTGACATCTTGACAGCATACTGATGAGAGATGCTTAAACAGACTTCAGCCAG 728
DB 105 GlyIleArgThrGlyPheLeuLysIleAspGluTyrMetArgAsnPheSerAspLeuArg 124
QY 729 AAGCTGCTGAGAAAGATGGTCCACTGCCAGGTGTGTTCTGCTGTAGACAACTTCTT 788
DB 125 AsnGlyMetAspArgSerGlySerThrAlaValGlyValMetIleSerProLysHisIle 144
QY 789 TATATTGCAACCTCGAGATAGTGGGCAATCTTGATGATATATGAGAGAGAGTCAA 848
DB 145 TyrPheIleAsnGlySerIleAspSerArgAlaValLeuTyrArgAsnGlyGln----- 161

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QY 849 AATCATGACCTTAAGCTTCAGCAAGAGATTAATCCAACTAGTATGAGAGCCGATG 908
DB 162 -----ValCysPheSerThrGlnAspHisLysProCysAsnProArgGluLysGlu 178
QY 909 AGGATACAAAGAGCTGGAGAGAAAGCTGAGGATGGCGGTTTGGGCGTGTAGAGGTG 968
DB 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
QY 969 TCAGCTCCATTTGGGAGACGGGCACTACAAAGCTGGCGT----- 1007
DB 199 SerArgAlaLeuGlyAspTyrAspTyrLysCysValAspGlyLysGlyProThrGluGln 218
QY 1008 ---GTACCTCTGTGCTCCGACATGACAGCTGCCAGCTCAAGCCCAATGACAGTTTAT 1064
DB 219 LeuValSerProGluProGluValTyrGluIleLeuArgAlaGluGluAspGluPheIle 238
QY 1065 TTGTGGCTGTGATGGGCTCTTCAGGTTTATCCCAAGAAAGCCGTGAACCTTCATC 1124
DB 239 IleLeuAlaCysAspGlyIleTyrAspValMetSerAsnGluGluLeuCysGluTyrVal 258
QY 1125 TTGTCTGTCTGAGAGATGAAAAGATCCAGACCCGGGAAAGGAGTCCGACGCGACCC 1184
DB 259 LysSerArgLeuGlu-----ValSerAsp 266
QY 1185 CGTACGAGAGACGCTCGACAGAGCTGACCAAGCGGTGTCAGCGGCTCGCCGAC 1244
DB 267 AspLeuGluAsnValCysAsnTyrValValAspThrCysLeuHisLysGlySerArgAsp 286
QY 1245 AACGTCACGTGTATGTGGTGTG 1265
DB 287 AsnMetSerIleValLeuVal 293

RESULT 13
US-09-206-646-1
/ Sequence 1, Application US/09206646
/ Patent No. 643637
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Lal, Preeti G.
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Zhang, Hong
/ TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
/ FILE REFERENCE: PF-0319-1 DIV
/ CURRENT APPLICATION NUMBER: US/09/206,646
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PERL Program
/ SEQ ID NO 1
/ LENGTH: 479
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 643637 013177CD1
US-09-206-646-1

Alignment Scores:
Pred. No.: 1,34e-23 Length: 479
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
Gaps: 8

US-09-935-124A-1 (1-1422) x US-09-206-646-1 (1-479)
QY 333 AAGAGAAAACCTCCGAGAGAGAGATGCGACGATGAGAGCTTGAGAAAAGAAATT 392
DB 7 LysProlyserThrGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
QY 393 TGTAAAGCCTCTCGGTATCTTTGTCTGAAGGGCTATGTGGCGGAGAGGTGAG 452

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Db 120 ValHisLeuGlnValGlyAlaValGlyAlaSerSerArgValAlaIcys----- 135
 QY 840 GAGAGTCAAAACATGACAGCCTTAAAGCTTCACGAAAGAGCACTAACTCACTCAATGATGAA 899
 Db 136 -----TLeaSpGlyValCysValProLeuTrnGluAspHisIleuSProMenhenuGluIly 153
 QY 900 GACCGGATGAGATACAGAAAGCTGAGGAAACCTCAGGATGGGCTGTGTTGGCGCTG 959
 Db 154 GluArgGlnArgIleGluAsnCyAlaGlyArgValGluAsnAsnArgValAspGlySer 173
 QY 960 CTAGAGTGTCACTGCTCCATTTGGGAGCGGCGAGTACAAAG----- 998
 Db 174 LeuAlaValSerArgAlaPheGlyAspArgGluTrpIleuGlySerGlySerGlnLeu 193
 QY 999 CGCTGGCGGTGTCACCTCTGTGCGCGACATCAGACCTGCTCCAGCTGACC-----CCCAAT 1052
 Db 194 GluGlnIleValIleAlaLeuAlaSerValGlnHisIleuAspPheTrpPheAspSerAsn 213
 QY 1053 GACAGGTCATTTGTTGGCTGTGATGAGGCTCTTCAAG--GTCCTTACCCGAGAGAA 1109
 Db 214 Asp---PheValIleuLeuCyCyAspArgIlyAlaPheGlnGluIleuPheProAsnGlnGlu 232
 QY 1110 GCGGTGAACCTCATCTGTCTGTCTGAGAGATGAAAAGATTCACAGACCGGAGGAGAG 1169
 Db 233 ValValAlaIleTrpValIleGlnGlnLeuGlu----- 242
 QY 1170 TCGGACGCGAGCGCCGCTGACGAGACCTGCAAC-----AGG 1208
 Db 243 -----ThCysAsnAspLeuAlaGluValAlaGlyArg 253
 QY 1209 CTGCGCCACAAAGCGGTGACAGCGGGCTGCGCCGACAAACGTCACTGATGATGGTGGCG 1268
 Db 254 ValCyAsnGlnGluAlaIleGluArgIleSerArgAspAsnIleSerCyMetIleValGln 273
 RESULT 15
 US-08-935-855-10
 / Sequence 10, Application US/08935855
 / Patent No. 6066485
 / GENERAL INFORMATION:
 / APPLICANT: Guthridge, Mark
 / APPLICANT: Basillico, Claudio
 / TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 / TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 / NUMBER OF SEQUENCES: 22
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: David A. Jackson, Esq.
 / STREET: 411 Hackensack Ave, Continental Plaza, 4th
 / STREET: Floor
 / CITY: Hackensack
 / STATE: New Jersey
 / COUNTRY: USA
 / ZIP: 07601
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/935,855
 / FILING DATE:
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Jackson Esq., David A.
 / REGISTRATION NUMBER: 26,742
 / REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 201-487-5800
 / TELEFAX: 201-343-1684
 / INFORMATION FOR SEQ ID NO: 10:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 314 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single

QY 1209 CTGGCCACAGCGGTGCGCGGGCTCGCCGACCACTGATGATGTCGG 1268
DB 254 ValcylglutunilalegluarglyserargaspamleiserCysmetileValGln 273

RESULT 16
US-08-822-701-2
Sequence 2, Application US/08822701
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Gueridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-08-822-701-2

Alignment Scores:
Pred. No.: 3,276-19 Length: 392
Score: 270.00 Matches: 109
Percent Similarity: 42.09% Conservative: 64
Best Local Similarity: 26.52% Mismatches: 147
Query Match: 10,554 Indels: 91
DB: 2 Gaps: 18

US-09-935-124a-1 (1-1422) x US-08-822-701-2 (1-392)

QY 77 CTGCGCCCTTCACCCAGCTCCGCGCATGACCTTTGCGGAGCTCGCGAGCCGAGCG 136
DB 17 ValProPro-HisThrIysSerGlyIleGlyThr---GlyAspGluProGlyProGln-- 34

QY 137 CTGCGCGCGCGCGGTGCGCGGAAAGAAAGCTCAAGAAAGACCCCTGCTCTTTGATGACCT 196
DB 35 -----GlyLeuAsnGlyGluAlaGlyPro-----GluAsp-- 44

QY 197 CCCTCGGCGCAGAGTACTGACTCAGGATCAGGGGAGCTTTGCTTTTGATGATCTCCC 256
DB 45 ----ProSerArgGluThrProSerGlnGluAsnGlyProThrAlaLysGlyHisThrGln 63

QY 257 ACCCGCTAGCAGTGGCGATTCAAGTTCTCTTGCCACATCATATCCAGATGTAAAGAC 316

DB 63 yheserSerAsnSerGluHisGlyThrGluAlaGlyGlnIleSerGluProGlyThrAl 83
QY 317 TGAAGGAAAGAGCAAGAAAGAAAACTCCGAGGAAGAGAAATGCGATGAAGAGCT 376
DB 83 aThrGlyGluAlaGlyProSerCysSerSerAlaSerAspLys----- 97

QY 377 TGTGAAAAGAAAGTTGTAAAGCTCTTCGCGTGAATCTTTGCTGAAAGGCTATGTGC 436
DB 98 ----LeuProArgValAlaLysSerLys-----PhePheGln 108

QY 437 TGAAGCGAAGGTGAGAGGAGAGATGCGATGCCATCTCATCTGAAGCATC 496
DB 108 uAspSerGluAspGluSerAspGluValGlnGlu-----GluAspAspSe 124

QY 497 CGAGAGGTAGAGCCCGCATGCTCCCTCATTACTCGGGTTTCATATTTGCTGTTTGA 556
DB 124 rGluGluCysSerGluAspGlu-----As 132

QY 557 TGAACATGAGAGAAATTCAGACCTCAAAATTTGCTGACAGAAATTTGCATCAAACTTAAT 616
DB 132 pGlyTyr-----SerSerGluGluAlaGluAsn----- 141

QY 617 CAGAAAATTCTTAAGAGATGTATCAGTGAAGAAACCGTGAAGATGCTTTT 676
DB 142 ---GluGluAspGluAspAspThrGluGluAlaGlu----- 152

QY 677 GGACACTTCAGCATACTGATGAAGAGTCTT-----AAACAAGCTTCCAGCAGAA 730
DB 153 -----GluAspAspAspGluGluMetValProGlyMetGluGlyGlyGluGln 169

QY 731 GCGTCGCTGGAAGATGGGTCCACTGCCAGCGTGTCTGCGCTGAGCAACATCTTTA 790
DB 169 uProGlySerAspSerGlyThrThrAlaValAlaLeuIleArgGlyLysGlnLeuI 189

QY 791 TATTGCCAATCTCGAGATATGCGGCAATCTTGCTGTGTTAATGAGAGATCAAA 850
DB 189 eValAlaAsnAlaGlyAspSerArgCysValVal-----SerGluAla 203

QY 851 ACATGACGCTTAAGCTCAGCAAGCAAGATTAATCAATCAGTGAAGAGCGAGTGA 910
DB 203 aGlyLysAlaLeuAspMetSerTyrAspHisLeuProGluAspGluValGluLeuAlaTr 223

QY 911 GATACAGAAGCTGAGAGGAACGTC---AGGATGAGCGGTGTTTGCGCTGCTAGAGT 967
DB 223 gIleLysAsnAlaGlyGlyLysValThrMetAspGlyArgValaAsnGlyGlyLeuAsnLe 243

QY 968 GTACGCTTCATTGGGAGCGGAGCATACAGCGCTGCGGT----- 1007
DB 243 uSerArgAlaIleGlyAspHisPheTyrLysArgAsnLysAsnLeuProProGlnGluGln 263

QY 1008 ----GTACGCTGTGCGCGCATCAGACGCTGCCAGCGTGAACCCCATGACAGGTTAT 1063
DB 263 mMetIleSerAlaLeuProAspPheLysValLeuThrLeuThrAspAspHisGluPhe 283

QY 1064 TTTGTGCGCTGTGATGGCTCTTCAAGGCTTTTACCCAGAAAGAGCGGTGAACCTCAT 1123
DB 283 tValIleAlaCysAspGlyIleTyrAsnValMetSerSerGlnGluValaAspPhe 303

QY 1124 CTGTGCTGTCTC-----GAGGATGAAGATCCAGACCCGGAAGGAAAGTCCGACAG 1177
DB 303 eGlnSerLysIleSerGlnArgAspGluAsnGlyLutLeuArgLeuLeuSerSerIleVal 323

QY 1178 CGAGCCCGCTACAGAGCAGCTGCAACAGCTGCGCCAAAGAGCGGTGACCGGGGCTC 1237
DB 323 LGIU-----GluLeuLeuAspGlnCysLeuAlaProAspThrSerGlyAspGlyTh 340

QY 1238 G---GCCGACAGCTCACTGTGATGTGTG 1265
DB 340 rGlyCysAspAsnMetThrCysIleIleIle 350

RESULT 17
US-08-935-855-2

Sequence 2, Application US/08935855

Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark

APPLICANT: Basilio, Claudio

TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESS: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR: Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,855

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION: David A.

NAME: Jackson Esq., 26, 742

REGISTRATION NUMBER: 1049-1-002 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-467-1684

TELEFAX: 201-467-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 392 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

FRAGMENT TYPE: N-terminal

US-08-935-855-2

Alignment Scores:

Pred. No.: 3,276-19

Score: 270.00

Percent Similarity: 42.09%

Best Local Similarity: 26.52%

Query Match: 10.55%

DB: 3

Length: 392

Matches: 109

Conservative: 64

Mismatches: 147

Indels: 91

Gaps: 18

US-08-935-124A-1 (1-1422) x US-08-935-855-2 (1-392)

QY 77 CTGCGCCCTCCACCCAGCTTCGCGCATGAGACTTCGCGGAGCTGCGGAGCCCGAGCG 136

DB 17 ValProPro-HisThrLysSerGlyIleGlyThr--GlyAspGluProGlyProGln-- 34

QY 137 CTCGCGCGCGCGCGCTGCGGAGAAAGAGTCCAGAAAGAGCCCTGCTTTGATGACT 136

DB 35 -----GlyLeuasnGlyGluAlaIleGlyPro-----GluAsp-- 44

QY 197 CCCTCCGCGCAGAGTACTGACTCAGATCAGATCAGGCGGAGCTTGTCTTTGATGATCTCC 256

DB 45 -----ProSerArgGluThrProSerGlnGluAsnGlyProThrAlaLysGlyHisThrG1 63

QY 257 ACCCGTAGAGAGTGGAGATTCAGGTTCTCTTGCACATCAATATCCAGATGCTAAAGAC 316

DB 63 yPheSerSerAsnSerGluHisGlyThrGluAlaGlyGlnIleSerGlnProGlyThrAl 83

QY 317 TGAAGGAG 376

DB 83 aThrGlyGluAlaIleGlyProSerGlySerSerAlaSerAspLys----- 97

QY 377 TGTGAGAAAG 430

DB 98 -----LeuProArgValAlaLysSerLys-----PhePheG1 108

QY 437 TGAAGGAG 496

DB 108 uAspSerGluAspGluSerAspGluValGluGluGlu-----GluAspAspSe 124

QY 497 CGAGAGAGTGAAGCGCCCACTCTCCCTCATTACTCGGAGTTTCAATATTTTGGCTGTTTTGA 556

DB 124 rGluGluLysSerGluAspGlu-----As 132

QY 557 TGAAG 616

DB 132 polyLys-----SerSerGluGluAlaGluAsn----- 141

QY 617 CAGAAATTTCTTAAGAGAGATGTATATAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 676

DB 142 -----GluGluAspGluAspThrGluGluAlaGlu----- 152

QY 677 GAGACACTTCAAGCATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730

DB 153 -----GluAspAspAspGluGluLysMetCysAlaProGlyMetGluGlyLysGluG1 169

QY 731 GCCTGCTGAG 790

DB 169 uProGlySerAspSerGlyThrThrAlaValAlaLeuIleArgGlyLysGluMetI1 189

QY 791 TATGCGCAACTCCGAGATAGTGGCGCATCTTGCTGCTTATATAGAGAGAGAGAGAGAGAG 850

DB 189 eValAlaAsnAlaGlyAspSerArgCysVal-----SerGluAl 203

QY 851 ACATGAGAGCTTAAGCTTCAG 910

DB 203 aGlyLysAlaLeuAspMetSerLysThrAspProGluAspGluValGluLeuAlaAr 223

QY 911 GATACAG 967

DB 223 gIleLysAsnAlaGlyGlyLysValIleMetAspGlyLysGlyAlaAsnGlyLysLeuAsnLe 243

QY 968 GTACGCTTCATTTGGAG 1007

DB 243 uSerArgAlaIleGlyAspHisPheThrLysArgAsnLysAsnLeuProGlnGluG1 263

QY 1008 -----GTACCTGTGTGCGCCGACATTCAGAGAGCTGACAGCTGACCCCAATGACAGTAT 1063

DB 263 mMetIleSerAlaLeuProAspLysValLeuThrLeuThrAspPheHisGluPheMe 283

QY 1064 TTTGTTGGCTGTGATGGGCTCTTCAAGGCTTTTACCCAGAGAGAGAGAGAGAGAGAGAGAG 1123

DB 283 tValIleAlaCysAspGlyIleThrAsnValMetSerSerGlnValAlaAspPheI1 303

QY 1124 CTGTGCTGTCTC-----GAGATGAGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1177

DB 303 eGlnSerLysIleSerGlnArgAspGluAsnGlyGluLeuArgLeuSerSerIleLea 323

QY 1178 CAGAGCGCCCTGAG 1237

DB 323 tGlu-----GluLeuLeuAspGlnCysLeuAlaProAspThrSerGlyAspLysTh 340

QY 1238 G-----GCCAGACAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265

DB 340 rGlyCysAspAsnMetThrCysIleIleIle 350

RESULT 18

US-08-935-855-22

Sequence 22, Application US/08935855

Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark

APPLICANT: Basilio, Claudio

TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-144-178-2

Alignment Scores:
Pred. No.: 1,21e-09 Length: 504
Score: 178.00 Matches: 83
Percent Similarity: 40.88% Conservative: 65
Best Local Similarity: 22.93% Mismatches: 116
Query Match: 6.95% Indels: 98
Gaps: 18

US-09-935-124a-1 (1-1422) x US-09-144-178-2 (1-504)

QY 330 GCAAGAGAGAAAACC-----TCGAGAGAGAGAGAGATGCGATGAAGAGCTTTG 380
DB 3 AlAGlnArgSerLeuInSerGlnInProSerTrpThrAspLeu--- 21
QY 381 GAAAGAAAGTTGTAAAGCCTTCCTCGATG---ATCTTGTCTGAAGAGGCTATGTGCT 437
DB 22 -----ProLeuGlySerLeuSerGlyValGlySerAlaSerAspArgSerTyrSerAla 39
QY 438 GAGCGAAGGGGTGAGAGGAGAGATGCGAGATGCCACGTCATCTGAACGATCAC 497
DB 40 AspGlyLeuSerGly-----Thr 44
QY 498 GAGAGGTAGCGCCCATCGTCCTCAT---ACTCGGTTTCATAT 542
DB 45 GluSerHisProProGlnAspSerTrpLeuLysPheArgSerGluAsnAsnCyPheLeu 64
QY 543 TTTCCTGTTTGTATGACATGAGAGATTCGAGCCCAAAATTTGCGACAGATTTG 602
DB 65 TyrGlyValPheAsnGlyTyrAspGlyAsnArgValThrAsnPheValAlaGlnArgLeu 84
QY 603 CATCAAACTTAATCAGAAAATTTCTTAAAGAGATGTAATCAGTGTAGAGAAACCGTG 662
DB 85 SerAlaGluLeuLeu-----LeuGlyGlnLeuAsnAlaGluHisAlaGlnAlaAspVal 102
QY 663 AAGAGATGCCTTTGTGACACTTTCAGACATCTGATGAGAGATTTCTT 710
DB 103 ArgArgValLeuLeuGlnAlaPheAspValValGlnArgSerPheLeuGlnSerIleAsp 122
QY 711 -----AAACAAGTTTCAGCCAGAG----- 721
DB 123 AspAlaLeuAlaGlnLysAlaSerLeuGlnSerGlnLeuProGlnGlyValProGlnHis 142
QY 732 -----CCTGCTCGAAA----- 743
DB 143 GlnLeuProGlnTyrGlnLysIleLeuGlnArgLeuLysThrLeuGlnArgGlnIle 162
QY 744 ---GATGGTCCACTGCCAGGTGTCTGCTGCTGACAGCAATCTTTATATTGCCAAC 800
DB 163 SerGlyGlyAlaMetAlaValAlaValAlaValLeuLeuAsnLysLeuTyrValAlaAsn 182
QY 801 CTCGAGATGATCGGCAATCTGTGCTGTTATGATGAGAGAGTCAAAAGATGCACACC 860
DB 183 ValGlyThrAsnArgAlaLeuLeuGlyLysSerThrValAspGlyLeuGln-----Val 200

QY 861 TTAAGCTCAGAAAGAGATATCCAACTCAGTATGAGAGCGATGAGATACAGAG 920
DB 201 ThrGlnLeuAsnValAspHisThrArgLysAsnGlnLysAspGlnLeuPheArgLeuSerGln 220
QY 921 GCTTGA-----GGAAACGTCAGAGATGGGCGCTTTGGCGCTGTACAGGTGCA 971
DB 221 LeuGlyLeuAspAlaGlyLysIleLeuGlnValGlyIleLeuGlnLysGlnLeuThr 240
QY 972 CCTCATTTGGGAGCGGAGCAAG---CGCGCGGTGCACCTCTGTG----- 1019
DB 241 ArgArgIleGlyAsp-----TyrIysValLysTyrGlyTyrThrAspIleAspLeuLeu 258
QY 1020 -----CCGACATCAGACGCTGCCAGTCAAC 1046
DB 259 SerAlaAlaLysSerLysProIleIleAlaGlnProGlnLysGlnValAlaGln----- 276
QY 1047 CCCATGAC-----ACGTCATTTGTGTGCGCTGTATGAGCGCTTCAGAGTCTT 1097
DB 277 ProLeuAspGlyValThrGlyPheLeuValLeuMetSerGlnGlyLeuTyrLysAlaLeu 296
QY 1098 ACC-----CCGAAAGAGCGGTGAACCTTCATCTTGTCTGTCTCCAGATGA 1145
DB 297 GluAlaAlaAsnArgProGlyGlnAlaAsnGlnLysIleAlaAlaMetIleAspThrGln 316
QY 1146 AAGATCAGACCCGGGAAAGGAAAGTCCGACGCCGCTACGAGAGCGCTGCAAC 1205
DB 317 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValaAsp 332
QY 1206 AGGCTG 1211
DB 333 ArgVal 334

RESULT 22
US-09-406-854-2
Sequence 2, Application US/09406854
Patent No. 6140042
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiko
INVENTOR: NISHIDA, Etsuke
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,854
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 504 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-406-854-2

Alignment Scores:
Pred. No.: 1,21e-09      Length: 504
Score: 178.00           Matches: 83
Percent Similarity: 40.88%  Conservative: 65
Best Local Similarity: 22.93%  Mismatches: 116
Query Match: 6.95%       Indels: 98
DB: 4                   Gaps: 18

US-09-935-124A-1 (1-1422) x US-09-406-854-2 (1-504)

Qy 330 GCAAGAGAAAAAC-----TCCGAGAGAGAGAGATGCGATGAGAGCTTGTG 380
Db 3 AlaGlnArgArgSerLeuLeuGlnSerGlnGlnProSerTrpThrAspLeu--- 21
Qy 381 GAAAAGAAAGTTGTAAAGCCTTCGCGTG---ATCTTGTGTGAAGGCGTATGTGGCT 437
Db 22 -----ProLeuCyHisLeuSerGlyValGlySerAlaSerAsnArgSerTyrSerAla 39
Qy 438 GAGCGAAAGGTGAGAGGAGAGATGCGAGATGCCACGTATCCTGAACGATCAACC 497
Db 40 AspGlyLysGly-----Thr 44
Qy 498 GAGAGGTGAGGCCCCCATCGCTCATTT-----ACTCGGCTTTCATAT 542
Db 45 GluSerHisProProGlnAspSerTrpLeuLysPheArgSerGluAsnAsnCysPheLeu 64
Qy 543 TTTCGTGTTTTGATGACATGAGAGAAATTCGAGCCTCAAAATTTGCTGCAGAAATTTG 602
Db 65 TyrGlyValPheAsnGlyTyrArgPheAsnArgValThrAsnPheValAlaGlnLysAlaAsn 84
Qy 603 CATCAAACTTAATCAGAAATTTCTTAAAGGAGATGTAATCAGTGTAGAGAAACCGTG 662
Db 85 SerAlaGluLeuLeu-----LeuGlyGlnLeuAsnAlaGlnHisAlaGlnLysAlaAsn 102
Qy 663 AAGAGATGCTTTTGACACCTTTCAGGCACTACTGATGAAGATTCCTT----- 710
Db 103 ArgArgValLeuLeuGlnAlaPheAsnArgValValGluArgSerPheLeuGluSerLeuAsp 122
Qy 711 -----AAACAGCTTCAGCCAGANG----- 731
Db 123 AsnAlaLeuAlaGlnLysAlaSerLeuGlnSerGlnLeuProGluGlyValProGlnHis 142
Qy 732 -----CCTGCTCGGAAA----- 743
Db 143 GlnLeuProGlnTyrGlnLysIleLeuGluArgLeuLysThrLeuGlnLysArgLysIle 162
Qy 744 ---GATGGGTCCATGCGCCACGTGTGTTCTGCGCTGAGACACATTTTATATTCGCAAC 800
Db 163 SerGlyGlyAlaMetAlaValAlaValLeuLeuAsnAsnLysLeuTyrValAlaAsn 182
Qy 801 CTCGAGATAGTCGGGCAATCTTGTCGTTTATATGAGAGAGCAAAAACATCAGCC 860
Db 183 ValGlyThrAsnArgAlaLeuLeuCyHisLysSerThrValAspGlyLeuGln-----Val 200
Qy 861 TTAAGCCTCAGCAAGACATATCAACTCAGTATGAAGAGCGGATGAGATCAGAAAG 920
Db 201 ThrGlnLeuAsnValAspHisThrThrGluAsnGluAspGluLeuPheArgLeuSerGln 220
Qy 921 CCTGGA-----GAAACGTCAGGATGGCGCTGTTTGGCGCTGAGAGGTGCA 971
Db 221 LeuGlyLeuAsnArgAlaGlyLysIleLysGlnValGlyIleLeuCyGlyGlnLysSerThr 240
Qy 972 CGCTCCATTTGGGAGAGGCGCATGACAG---CGCTCGGTGTACCTCTGTG----- 1019
Db 241 ArgArgIleGlyAsp-----TyrLysValLysTyrGlyTyrThrAspIleAsnLeuLeu 258

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Qy 1020 -----CCGACATCAGACGCTGCCAGCTGACC 1046
Db 259 SerAlaAlaLysSerLysProIleLeuAlaGluProGluIleHisGlyAlaGln----- 276
Qy 1047 CCCATGAC-----AGGTTCATTTTGTGGCCTGTGATGGCTTTCAAGCTCTTT 1097
Db 277 ProLeuAspGlyValThrGlyPheLeuValLeuMetSerGluGlyLeuTyrLysAlaLeu 296
Qy 1098 ACC-----CCAGAGAAAGCCGTGAACCTTCATCTTGTCTGCTCGAGAGATGAA 1145
Db 297 GluAlaAlaHisGlyProGlyGlnHisAsnGlnGluIleAlaAlaMetIleAspThrGlu 316
Qy 1146 AAGATCCAGACCCGGGAGAGGAGATCCGACCGACCGCCGCTGACAGACCTGCAC 1205
Db 317 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValAlaAsp 332
Qy 1206 AGCGTG 1211
Db 333 ArgVal 334

RESULT 23
US-09-529-279-2
; Sequence 2, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIOHKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-279-2

Alignment Scores:
Pred. No.: 1,21e-09      Length: 504
Score: 178.00           Matches: 83
Percent Similarity: 40.88%  Conservative: 65
Best Local Similarity: 22.93%  Mismatches: 116
Query Match: 6.95%       Indels: 98
DB: 4                   Gaps: 18

US-09-935-124A-1 (1-1422) x US-09-529-279-2 (1-504)

Qy 330 GCAAGAGAAAAAC-----TCCGAGAGAGAGAGATGCGATGAGAGCTTGTG 380
Db 3 AlaGlnArgArgSerLeuLeuGlnSerGlnGlnProSerTrpThrAspLeu--- 21
Qy 381 GAAAAGAAAGTTGTAAAGCCTTCGCGTG---ATCTTGTGTGAAGGCGTATGTGGCT 437
Db 22 -----ProLeuCyHisLeuSerGlyValGlySerAlaSerAsnArgSerTyrSerAla 39
Qy 438 GAGCGAAAGGTGAGAGGAGAGATGCGAGATGCCACGTATCCTGAACGATCAACC 497
Db 40 AspGlyLysGly-----Thr 44
Qy 498 GAGAGGTGAGGCCCCCATCGCTCATTT-----ACTCGGCTTTCATAT 542
Db 45 GluSerHisProProGlnAspSerTrpLeuLysPheArgSerGluAsnAsnCysPheLeu 64
Qy 543 TTTCGTGTTTTGATGACATGAGAGAAATTCGAGCCTCAAAATTTGCTGCAGAAATTTG 602

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Db      65 TyrGlyValPheAenGlyTyrAspGlyAenArgValThrAenPheValAlaGlnArgLeu 84
Qy      603 CATCAAACTTATACAGAAAATTTCTTAAGAGATGTAATCATGTAGAGAAAACCGG 662
Db      85 SerAlaGlnLeuLeu-----LeuGlyGlnLeuAenAlaGlnHisAlaGlnAlaAspVal 102
Qy      663 AAGAGATGCTTTTGGACACTTTCAGACATCTAGTGAAGAGTTCCCTT----- 710
Db      103 ArgArgValLeuLeuGlnAlaPheAspValValGlnArgSerPheLeuGlnSerIleAsp 122
Qy      711 -----AAACAAGCTTCAGCCAGAAAG----- 731
Db      123 AspAlaLeuAlaGlnLysAlaSerLeuGlnSerGlnLeuProGlnGlyValProGlnHis 142
Qy      732 -----CCTGCTGGAAA----- 743
Db      143 GlnLeuProProGlnTyrGlnLysAlaLeuGlnLysArgLeuLysThrLeuGlnLysGlnLe 162
Qy      744 ---GATGGGTCCACTGCGCATGTGTCTGCTGTAGACAACATTTCTTATATTGGCAAC 800
Db      163 SerGlyGlyAlaMetAlaValAlaValAlaValLeuLeuAenAenLysLeuTyrValAlaAen 182
Qy      801 CTGGAGATAGTCGGGCAATCTGTGTCGTTATATAGAGAGAGTCAAAAACATGCAGCC 860
Db      183 ValGlyThrAsnArgAlaLeuLeuLeuCysLysSerThrValAspGlyLeuGln-----Val 200
Qy      861 TTAAAGCTCAGCAAGACATATATCCAACTCAGTATGAAAGCGGATGAGATACAGAG 920
Db      201 ThrGlnLeuAenValAspIleThrThrGlnAenGlnAspGlnLeuPheArgLeuSerGln 220
Qy      921 GCTGGA-----GAAACGTCAGAGATGGCGCTTTTGGCGCTGTAGAGTGTCA 971
Db      221 LeuGlyLeuAspAlaGlyLysIleLeuGlnValGlyIleIleCysGlyGlnHisSerThr 240
Qy      972 CGCTCCATTGGGACCGGACAGTACAG---CGCTCGGCTGTCACTCTGTG----- 1019
Db      241 ArgArgIleGlyAsp-----TyrLysValLysTyrGlyTyrThrAspIleAspLeuLeu 258
Qy      1020 -----CCGACATCAGACGCTGCACGCTGACC 1046
Db      259 SerAlaLysSerLysProIleIleAlaGlnProGlnIleHisGlyAlaGln----- 276
Qy      1047 CCCAAATGAC-----AGTTCAATTTTGGCTGAGTGGATGGGCTCTCAAGTCTTT 1097
Db      277 ProLeuAspGlyValThrGlyPheLeuValLeuMetSerGlnGlyLeuTyrIleAlaLeu 296
Qy      1098 ACC-----CCAGAAGAGCGGTGAACCTTCACTTTCCTGCTGCTGAGAGTGA 1145
Db      297 GlnAlaAlaHisGlyProGlyGlnAlaAenGlnIleAlaAlaMetIleAspThrGln 316
Qy      1146 AAGATCCAGACCGGAGAGAGATCCGACCGACCGACCGCTACAGAACGCTGCAGAC 1205
Db      317 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValAlaAsp 332
Qy      1206 AGGCTG 1211
Db      333 ArgVal 334

RESULT 24
US-09-529-279-43
; Sequence 43, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188

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; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-529-279-43

Alignment Scores:
Pred. No.: 1,23e-09 Length: 513
Score: 178.00 Matches: 83
Percent Similarity: 40.88% Conservative: 65
Best Local Similarity: 22.93% Mismatches: 116
Query Match: 6.95% Indels: 98
DB: Gaps: 18

US-09-935-124a-1 (1-1422) x US-09-529-279-43 (1-513)
Qy      330 GCAAAGAGAAAACC-----TCCAGAGAAAGAAAGATGCGAGAGAGTGTG 380
Db      12 AlaGlnArgSerLeuLeuGlnSerGlnGlnGlnProSerThrIleAspLeu---- 30
Qy      381 GAAAGAAAATTGTAAAGCTCTTGGGTC--ATTTGGTCTGAAGGCTATGGGCT 437
Db      31 -----ProLeuCysHisLeuSerGlyValGlySerAlaSerAsnArgSerIleAsp 48
Qy      438 GAGCGAAGAGGTGAGAGGAGAGAGATGACAGATGCCATGCTGAAACATCACC 497
Db      49 AspGlyLysGly----- 53
Qy      498 GAGAGGTGAGGCCCCCATCTGTCCTCATT-----ACTGGGTTTCATAT 542
Db      54 GlnSerHisProProGlnLysAspSerThrLeuLysPheArgSerGlnAenCysPheLeu 73
Qy      543 TTTCGCTTTTGGATGAGACATGAGAGAAATTCAGACCTCAAAATTTGTGCAAGATTTG 602
Db      74 TyrGlyValPheAenGlyTyrAspGlyAsnArgValThrAsnPheValAlaGlnArgLeu 93
Qy      603 CATCAAACTTATACAGAAAATTTCTTAAGAGATGTAATCATGTAGAGAAAACCGT 662
Db      94 SerAlaGlnLeuLeu-----LeuGlyGlnLeuAenAlaGlnHisAlaGlnAlaAspVal 111
Qy      663 AAGAGATGCTTTTGGACACTTTCAGACATCTAGTGAAGAGTTCCTT----- 710
Db      112 ArgArgValLeuLeuGlnAlaPheAspValAlaGlnArgSerPheLeuGlnSerIleAsp 131
Qy      711 -----AAACAAGCTTCAGCCAGAAAG----- 731
Db      132 AspAlaLeuAlaGlnLysAlaSerLeuGlnSerGlnLeuProGlnGlyValProGlnHis 151
Qy      732 -----CCTGCTGGAAA----- 743
Db      152 GlnLeuProProGlnTyrGlnLysAlaLeuGlnLysArgLeuLysThrLeuGlnLysGlnLe 171
Qy      744 ---GATGGGTCCACTGCGCATGTGTCTGCTGTAGACAACATTTCTTATATTGGCAAC 800
Db      172 SerGlyGlyAlaMetAlaValAlaValAlaValLeuLeuAenAenLysLeuTyrValAlaAen 191
Qy      801 CTGGAGATAGTCGGGCAATCTGTGTCGTTATATAGAGAGAGTCAAAAACATGCAGCC 860
Db      192 ValGlyThrAsnArgAlaLeuLeuLeuCysLysSerThrValAspGlyLeuGln-----Val 209
Qy      861 TTAAAGCTCAGCAAGACATATCCAACTCAGTATGAAAGCGGATGAGATACAGAG 920
Db      210 ThrGlnLeuAenValAspIleThrThrGlnAenGlnAspGlnLeuPheArgLeuSerGln 229
Qy      921 GCTGGA-----GAAACGTCAGAGATGGCGCTTTTGGCGCTGTAGAGTGTCA 971
Db      230 LeuGlyLeuAspAlaGlyLysIleLysGlnValGlyIleIleCysGlyGlnHisSerThr 249
Qy      972 CGCTCCATTGGGACCGGACAGTACAG---CGCTCGGCTGTCACTCTGTG----- 1019

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Db 250 ArgAaGIIeGIyAsp-----TyrIySValIySTyrGIYTrThrAspIleAspLeuLeu 267
Qy 1020 -----CCGAGATCAGACGCTGCCAGCTGACC 1046
Db 266 SerAlaAlaIySerIySerpIleIleAlaGluProGluIleHisIleGIyAlaGln----- 285
Qy 1047 CCCAATGAC-----AGGTTCAATTTGTTGGCTGTGATGGCTCTTCAAGGCTCTT 1097
Db 286 ProLeuAspGIyValThrGIyPheLeuValIleuMetSerGIuGIyLeuTyrIySAlaLeu 305
Qy 1098 ACC-----CCAGAGAGCCGGTGAACCTTCATCTTCGCTGCTCCAGAGATGAA 1145
Db 306 GluAlaAlaHisGIyProGIyGlnAlaAsnGlnIleIleAlaIleMetIleAspThrGIu 325
Qy 1146 AAGATCCAGACCCGGAGAGGAGTCCGACGCCGACCCGCTACAGACAGCTGCAAC 1205
Db 326 PheAlaIyS-----GlnThrSerIleuAspAlaValAlaGlnAlaValaIyAsp 341
Qy 1206 AGGCTG 1211
Db 342 ArgVal 343

RESULT 25
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-11

Alignment Scores:
Pred. No.: 1,236-09 Length: 517
Score: 178.00 Matches: 83
Percent Similarity: 40.88% Conservative: 65
Best Local Similarity: 22.93% Mismatches: 116
Query Match: 6.95% Indels: 98
DB: 4 Gaps: 18

US-09-935-124A-1 (1-1422) x US-09-529-279-11 (1-517)
Qy 330 GCAAGAGAGAAAAAC-----TCCGAGAGAGAGAAATGACGATGAGAGCTGTG 380
Db 3 AAGGlnAArgSerIleuGlnSerIleuGlnGlnIleProSerTrpThrAspLeu---- 21
Qy 381 GAAAAAGAAAGTTTGAACCTCTTCGCTG---AATCTTGCTGAAGGCTATGTGCT 437
Db 22 -----ProLeuCyHisIleuSerGIyValGIySerAlaSerAsnArgSerTyrSerAla 39
Qy 438 GAGCGGAGGCTGAGAGGAGAGAGATGCAGATGCCACGTCATCTCTGAACGATCAAC 497
Db 40 AspGIyIySgIy-----Thr 44
Qy 498 GAGAGTGTAGGCCCCCATCGTCCCTCATTT-----ACTCGGCTTCATAT 542
Db 45 GluSerHisIleProGlnAspSerTrpLeuIyS-PheArgSerGIuAsnAsnCySerpLeu 64
Qy 543 TTTGCTGTTTGTATGACATGAGAGAAATTGAGCTCAAAATTGCTTCAGAAATTTG 602

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Db 65 TyrGIyValPheAsnGIYTrYrAspGIyAsnArgValIThrAsnPheValAlaGlnThrGlu 84
Qy 603 CATCAAACTTAATCAGAAAAATTTCTTAAGAGAGATGATCAGTGTGAGAAAAACCGT 662
Db 85 SerAlaGluLeu-----LeuGIyGlnLeuAsnAlaGluHisAlaGluAlaAspVal 102
Qy 663 AAGAGATGCTTTTGAACATTTCAAGCATACGTATGAAAGATTCCTT----- 710
Db 103 ArgGIyValIleuGlnAlaPheAspValValGIuArgSerPheLeuGluSerIleAsp 122
Qy 711 -----AAACAAGCTTCCAGCCAGAG----- 731
Db 123 AspAlaIleuAlaGluIyAlaSerIleuGlnSerGlnLeuProGluGIyValProGlnHis 142
Qy 732 -----CCTGCCTGGAAA----- 743
Db 143 GlnLeuProProGlnTrpGlnIyS-IleLeuGIuArgLeuIySThrLeuGIuArgIuIle 162
Qy 744 --GATGGGTCCATGCCACGCTGTCTGCTGTGAGCAACATTTATTAATTTGCCAAC 800
Db 163 SerGIyGIyAlaMetAlaValAlaValaIleuLeuAsnAsnIleuTyrValAlaAsn 182
Qy 801 CTCGAGATAGTCGGGCAATCTTGCTGCTTAAATGAGAGAGTCAAAACATGCAACC 860
Db 183 ValGIyThrAsnArgAlaIleuLeuCySerpSerThrValAspGIyLeuGln-----Val 200
Qy 861 TTAACCTTCAGCAAGACATATCAACTCAGTATGAAAGCGGATGAGATACAGAG 920
Db 201 ThrGlnLeuAsnValAspHisIleThrThrGlnAsnGluAspGIuLeuPheArgLeuSerGln 220
Qy 921 GCTGA-----GAAACGTCAGGAGATGGCGCTGTTTGGGCGTCTAGAGGTGCA 971
Db 221 LeuGIyLeuAspAlaGIyIySerIleuGlnValGIyIleCyGIyGlnIuSerThr 240
Qy 972 CCTTCATTTGGGAGCGGACGATCAAG--CGCTCGGTGCACCTCTGTG----- 1019
Db 241 ArgAaGIIeGIyAsp-----TyrIySValIySTyrGIYTrThrAspIleAspLeuLeu 258
Qy 1020 -----CCGAGATCAGACGCTGCCAGCTGACC 1046
Db 259 SerAlaAlaIySerIySerpIleIleAlaGluProGluIleHisIleGIyAlaGln----- 276
Qy 1047 CCCAATGAC-----AGGTTCAATTTGTTGGCTGTGATGGCTCTTCAAGGCTCTT 1097
Db 277 ProLeuAspGIyValThrGIyPheLeuValIleuMetSerGIuGIyLeuTyrIySAlaLeu 296
Qy 1098 ACC-----CCAGAGAGCCGTGAACCTTCATCTTCTGCTGTGAGAGATGAA 1145
Db 297 GluAlaAlaHisGIyProGIyGlnAlaAsnGlnIleIleAlaIleMetIleAspThrGIu 316
Qy 1146 AAGATCCAGACCCGGAGAGGAGAGTCCGACGCCGACCCGCTACAGACAGCCGCAAC 1205
Db 317 PheAlaIyS-----GlnThrSerIleuAspAlaValAlaGlnAlaValaIyAsp 332
Qy 1206 AGGCTG 1211
Db 333 ArgVal 334

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Job time : 39.5 secs